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(54) Infection with chimaeric adenoviruses of cells negative for the adenovirus serotype 5
Coxsacki adenovirus receptor (CAR)

(57) The invention relates to the field of molecular genetics and medicine. The invention discloses a method for delivering a nucleic acid of interest to a host cell by means of a gene delivery vehicle based on adenoviral material, whereby said gene delivery vehicle delivers

the nucleic acid to the host cell by associating with a binding site and/or a receptor present on CAR-negative cells, said binding site and/or receptor being a binding site and/or a receptor for adenovirus subgroups D and/or F.

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Description

[0001] The invention relates to the field of molecular genetics and medicine. In particular the present invention relates to the field of gene therapy, more in particular to gene therapy using adenoviruses.

5 [0002] In gene therapy, genetic information is delivered to a host cell in order to either correct (supplement) a genetic deficiency in said cell, or to inhibit an unwanted function in said cell, or to eliminate said host cell. Of course the genetic information can also be intended to provide the host cell with a wanted function, for instance to supply a secreted protein to treat other cells of the host, etc.

10 [0003] Thus there are basically three different approaches in gene therapy, one directed towards compensating a deficiency present in a (mammalian) host; the second directed towards the removal or elimination of unwanted substances (organisms or cells) and the third towards providing a cell with a wanted function.

15 [0004] For the purpose of gene therapy, adenoviruses have been proposed as suitable vehicles to deliver genes to the host. Gene-transfer vectors derived from adenoviruses (so-called adenoviral vectors) have a number of features that make them particularly useful for gene transfer. 1) the biology of the adenoviruses is characterised in detail, 2) the adenovirus is not associated with severe human pathology, 3) the virus is extremely efficient in introducing its DNA into the host cell, 4) the virus can infect a wide variety of cells and has a broad host-range, 5) the virus can be produced at high virus titers in large quantities, and 6) the virus can be rendered replication defective by deletion of the early-region 1 (E1) of the viral genome (Brody et al, 1994).

20 [0005] However, there are still drawbacks associated with the use of adenoviral vectors especially the well investigated serotypes of subgroup C adenoviruses. These serotypes require the presence of the Coxsackie adenovirus receptor (CAR) on cells for successful infection. Although this protein is expressed by many cells and established cell lines, this protein is absent for many other primary cells and cell lines making the latter cells difficult to infect with serotypes 1, 2, 5, and 6.

25 [0006] The adenovirus genome is a linear double-stranded DNA molecule of approximately 36000 base pairs. The adenovirus DNA contains identical Inverted Terminal Repeats (ITR) of approximately 90-140 base pairs with the exact length depending on the serotype. The viral origins of replication are within the ITRs exactly at the genome ends.

30 [0007] Most adenoviral vectors currently used in gene therapy have a deletion in the E1 region, where novel genetic information can be introduced. The E1 deletion renders the recombinant virus replication defective (Levrero et al, 1991). It has been demonstrated extensively that recombinant adenovirus, in particular serotype 5 is suitable for efficient transfer of genes *in vivo* to the liver, the airway epithelium and solid tumours in animal models and human xenografts in immunodeficient mice (Bout, 1996; Blaese et al., 1995). Thus, preferred methods for *in vivo* gene transfer into target cells make use of adenoviral vectors as gene delivery vehicles.

35 [0008] At present, six different subgroups of human adenoviruses have been proposed which in total encompasses 51 distinct adenovirus serotypes. Besides these human adenoviruses an extensive number of animal adenoviruses have been identified (see Ishibashi et al, 1983).

40 [0009] A serotype is defined on the basis of its immunological distinctiveness as determined by quantitative neutralisation with animal antisera (horse, rabbit). If neutralisation shows a certain degree of cross-reaction between two viruses, distinctiveness of serotype is assumed if A) the hemagglutinins are unrelated, as shown by lack of cross-reaction on hemagglutination-inhibition, or B) substantial biophysical/ biochemical differences in DNA exist (Francki et al, 1991). The nine serotypes identified last (42-51) were isolated for the first time from HIV-infected patients (Hierholzer et al 1988; Schnurr et al 1993; De Jong et al 1998). For reasons not well understood, most of such immuno-compromised patients shed adenoviruses that were rarely or never isolated from immuno-competent individuals (Hierholzer et al 1988, 1992; Khoo et al, 1995, De Jong et al, 1998).

45 [0010] The adenovirus serotype 5 is most widely used for gene therapy purposes. Similar to serotypes 2, 4 and 7, serotype 5 has a natural affiliation towards lung epithelia and other respiratory tissues. In contrast, it is known that, for instance, serotypes 40 and 41 have a natural affiliation towards the gastrointestinal tract. For a detailed overview of the disease association of the different adenovirus serotypes see table 1. The underlying reason for the different natural affiliations of serotypes towards specific organs can be manifold. Such reasons may include but need not be limited to the observation that serotypes differ in the route of infection or make use of different receptor molecules or internalisation pathways or that a serotype can infect many tissues/organs but it can only replicate in one organ because of the requirement of certain cellular factors for replication. As mentioned before, it is presently unknown which mechanisms are responsible for the observed differences in human disease association.

50 [0011] One of the problems associated with the development of effective Gene Therapy protocols for the treatment of disease is the limitation of the current vectors to effectively transduce cells *in vivo*. One of the most effective ways to deliver foreign genetic material to cells *in vivo* is through the use of adenovirus vectors. Although, the vector system is very efficient the current adenovirus vector technology has its limitation. Specifically were certain cell types need to be transduced that are normally not very efficiently transduced by Adenovirus 2 or 5. Examples of such relatively resistant cell types include endothelial cells, smooth muscle cells, dendritic cells, neuronal cells, glial cells, synovical

cells, primary fibroblasts, cells from the amniotic fluid, hemopoietic stem cells, and monocytic/ macrophage cells etc. Thus in one aspect the invention provides a method for delivering a nucleic acid of interest to a host cell by means of a gene delivery vehicle based on adenoviral material, whereby said gene delivery vehicle delivers the nucleic acid to the host cell by associating with a binding site and/or a receptor present on CAR-negative cells, said binding site and/or receptor being a binding site and/or a receptor for adenovirus subgroups D and/or F. The method may advantageously be used to efficiently transduce cells both *in vitro* and *in vivo*.

5 [0012] The present invention was made during research with chimaeric adenoviruses. Said chimaeric adenoviruses comprising capsids derived from adenovirus 5 of which at least part of the adenovirus 5 fiber protein was replaced by a fiber protein from a different adenovirus serotype. It was observed that chimaeric adenoviruses comprising fiber 10 protein from adenovirus serotypes belonging to subgroup D or subgroup F were capable of efficiently transducing CAR negative target cells.

10 [0013] Adenovirus 2 and 5 belong to adenovirus subgroup C. Together with the adenoviruses of subgroups A, D-F, the subgroup C adenoviruses were before the present invention thought to attach to cells via the Coxsacki adenovirus receptor (CAR) (Roelvink et al, 1998).

15 [0014] It has been shown that adenoviruses of subgroup B such as Ad3 bind to a different receptor than CAR (Defer et al, 1990). Likewise, it was demonstrated that receptor specificity could be altered by exchanging the Ad3 with the Ad 5 knob protein, and vice versa (Krasnykh et al, 1996; Stevenson et al, 1995, 1997).

20 [0015] A host cell may be any host cell as long as it comprises a binding site and/or a receptor present on CAR-negative cells, said binding site and/or receptor being a binding site and/or a receptor for adenovirus subgroups D and/or F. Preferably, said cell is a human cell. Said cell may be a cell present in a culture dish or be part of a whole organism.

25 [0016] Preferably said CAR-negative cells are hemopoietic cells or amniotic fluid cells or derivatives thereof. Preferably, said CAR-negative hemopoietic cells are K562 cells. Preferably, said CAR-negative amniotic fluid cells are amniotic villi or chorion villi cells or derivatives thereof.

[0017] A gene delivery vehicle according to the invention may be any vehicle capable of transferring nucleic acid 30 into cells. Preferably, said gene delivery vehicle is a viral vector particle, more preferably said gene delivery vehicle is an adenoviral vector particle. The word gene in the term gene delivery vehicle does not reflect a situation wherein always an entire gene is delivered by said vehicle. The word gene in this respect merely reflects the presence of a nucleic acid of interest. Said nucleic acid may comprise an entire gene, an artificial sequence, a recombinant nucleic acid, a protein coding domain, a cDNA, a sequence coding for anti-sense RNA, mRNA and/or other kind of nucleic acid.

35 [0018] Suitable adenovirus material may comprise an adenovirus capsid or a functional part, derivative and/or analogue thereof. Said adenovirus capsid preferably comprises an adenovirus subgroup D or subgroup F capsid, or a functional part, derivative and/or analogue thereof. Said adenovirus capsid may also be a chimaeric capsid comprising proteins or parts thereof from at least two different adenovirus serotypes or derivatives and/or analogues thereof. Preferably, at least part of a fiber protein of said chimaeric capsid is derived from an adenovirus of subgroup D and/or subgroup F or a functional derivative and/or analogue thereof. Preferably, capsid proteins other than said part of a fiber protein, are derived from an adenovirus of subgroup C, preferably of adenovirus 5 or adenovirus 2. Suitable derivatives of said adenovirus capsids may, among other, be obtained through so-called silent amino-acid substitution in one or more capsid proteins.

40 [0019] Preferably, said adenovirus material comprises at least part of an adenovirus fiber protein. Preferably, said adenovirus fiber protein is derived from an adenovirus of subgroup D or subgroup F or a functional part, derivative and/or analogue thereof. Preferably, said part of a fiber protein is a part involved in binding to a receptor and/or a binding site on a target cell. Typically, but not necessarily said part of an adenovirus fiber protein involved in binding to a receptor and/or a binding site on a target cell is a part of the knob. Adenovirus fiber protein comprises at least three functional regions. One region, the base, is responsible for anchoring the fiber to a penton base of the adenovirus 45 capsid. Another region, the knob, is typically associated with receptor recognition whereas the shaft region functions as a spacer separating the base from the knob. Various regions may also have other functions. For instance, the shaft is presumably also involved in target cell specificity. Each of the regions mentioned above may be used to define a part of a fiber. However, regions of a fiber may also be identified in another way. For instance the knob region comprises of a receptor binding region and a shaft binding region. The base region comprises of a penton base binding region and a shaft binding region. Moreover, the shaft comprises of repeated stretches of amino acids. Each of these repeated 50 stretches may be a part.

A receptor and/or binding site binding part of a fiber protein may be a single region of a fiber protein or a functional part thereof, or a combination of regions or parts thereof of at least one fiber protein, wherein said receptor and/or binding site binding part of a fiber protein, either alone or in combination with one or more other proteins of a adenovirus 55 capsid, determines the efficiency with which a gene delivery vehicle can transduce a given cell or cell type, preferably but not necessarily in a positive way. Needless to say that said fiber and/or a capsid may comprise further modifications to adapt the fiber protein and/or the capsid to specific other needs, which a person skilled in the art will be capable of doing.

- [0020] A receptor and/or a binding site for adenovirus subgroups D and/or F may be any kind of molecule capable of associating with an adenovirus of subgroup D and/or F. In and/or on the surface of a cell, said receptor and/or binding site must be able to associate with said adenovirus of subgroup D and/or F provided to said cell. Said receptor and/or binding site may be part of a complex present in and/or on said cell. Said receptor and/or binding site does not need to be able to associate with an adenovirus of subgroup D and/or F all the time as long as it is capable of doing so some of the time. Said receptor and/or binding site may further also be a receptor and/or binding site for another virus and/or gene delivery vehicle, although this does not have to be so. A person skilled in the art may want to determine whether an adenovirus serotype belonging to another subgroup than D and/or F can also utilise the receptor and/or binding site for adenovirus subgroups D and/or F.
- [0021] In another aspect the invention provides the use of a gene delivery vehicle comprising a nucleic acid of interest and comprising adenoviral material involved in binding to a host cell, said material being from a subgroup D and/or F adenovirus, in delivering said nucleic acid of interest to a CAR-negative cell. With the knowledge of a novel pathway for the transduction of cells using adenovirus material it becomes possible to approach this novel pathway also through other means than said material derived from a subgroup D and/or F. A person skilled in the art recognises this and will be able to devise means to accomplish this for instance through the use of antibodies directed toward a crucial component of said pathway, together with a membrane fusion peptide. Such means and methods are also within the scope of the invention.
- [0022] In another aspect the invention provides a gene delivery vehicle being a chimaera based on at least two adenoviruses, whereby a cell recognising element of said gene delivery vehicle is based on adenoviral material from a subgroup D and/or F adenovirus, which material confers the capability of infecting CAR negative cells.
- [0023] Preferably, said adenoviral material is based on the fiber, penton and/or hexon proteins of a subgroup D and/or subgroup F adenovirus.
- [0024] To date, six different subgroups of human adenoviruses have been proposed which in total encompasses 51 distinct adenovirus serotypes. A serotype is defined on the basis of its immunological distinctiveness as determined by quantitative neutralisation with animal antisera (horse, rabbit). If neutralisation shows a certain degree of cross-reaction between two viruses, distinctiveness of serotype is assumed if A) the hemagglutinins are unrelated, as shown by lack of cross-reaction on hemagglutination-inhibition, or B) substantial biophysical/ biochemical differences in DNA exist (Francki et al, 1991). The nine serotypes identified last (42-51) were isolated for the first time from HIV-infected patients (Hierholzer et al 1988; Schnurr et al 1993;). For reasons not well understood, most of such immune-compromised patients shed adenoviruses that were rarely or never isolated from immune-competent individuals (Hierholzer et al 1988, 1992; Khoo et al, 1995, De Jong et al, 1998). The usefulness of these adenoviruses or cross-immunising adenoviruses to prepare gene delivery vehicles may be seriously hampered, since the individual to which the gene delivery vehicle is provided, will raise a neutralising response to such a vehicle before long.
- [0025] There is thus a need in the field of gene therapy to provide gene delivery vehicles, preferably based on adenoviruses, which do not encounter pre-existing immunity and/or which are capable of avoiding or diminishing neutralising antibody responses. Thus preferably, a gene delivery vehicle of the invention further comprises an element from adenovirus 35 or a functional equivalent thereof, responsible for at least partially avoiding an immune response against adenovirus 35. A functional equivalent/homologue of adenovirus 35 (element) for the purpose of the present invention is an adenovirus (element) which, like adenovirus 35, encounters pre-existing immunity in less than about 10% of the hosts, at least in a significant geographic region of the world, to which it is administered for the first time, or which is capable in more than about 90% of the hosts, at least in a significant geographic region of the world, to which it is administered to avoid or diminish the immune response. Typical examples of such adenoviruses are adenovirus serotypes 34, 26 and 48.
- [0026] In another embodiment a gene delivery vehicle according to the invention comprises an element of adenovirus 16 or a functional equivalent thereof, which element confers said virus with an enhanced capability to infect smooth muscle cells and/or synoviocytes. A functional equivalent of an element of adenovirus 16 in this respect is an element from another subgroup B virus. Preferably, said element is a tissue tropism determining part of a fiber protein. Typically, a tissue tropism determining part of an adenovirus fiber protein is a part that influences the transduction efficiency of a cell.
- [0027] For Gene Therapeutic purposes one typically does not want an adenovirus batch to be administered to a host cell which contains replication competent adenovirus, although this is not always true. In general therefor it is desired to omit a number of genes (but at least one) from the adenoviral genome on the vector encoding the virus and to supply these genes in the genome of the cell in which the vector is brought to produce adenovirus. Such a cell is usually called a packaging cell. The invention thus also provides a packaging cell for producing an adenovirus according to the invention, comprising *in trans*, all elements necessary for adenovirus production not present on the adenoviral vector according to the invention. Typically vector and packaging cell have to be adapted to one another in that they have all the necessary elements, but that they do not have overlapping elements which lead to replication competent virus by recombination. In a preferred embodiment said packaging cell is, or is derived from PER.C6 (ECCAC deposit number

96022940).

[0028] In another embodiment, a gene delivery vehicle according to the invention comprises an adenovirus vector. Said adenovirus vector may be a classical adenovirus vector, a minimal adenovirus vector or an integrating adenovirus such as an Ad/AAV chimaeric vector, a retro-adenovirus or a transposon-adenovirus or yet another different kind of adenovirus vector. With an integrating adenovirus vector for the purpose of the invention is meant a vector comprising nucleic acid derived from an adenovirus and further comprising means for the integration of at least part of the nucleic acid of said vector into the host cell genome. Said means are preferably derived from a nucleic acid with the inherent capacity to integrate into the host cell genome. Such nucleic acid with the inherent capacity to integrate into the host cell genome may be derived from a transposon or transposon-like element, a retrovirus and/or an adeno-associated virus or a different virus with the capacity to integrate nucleic acid into the host cell genome.

[0029] In a preferred embodiment said adenovirus vector comprises nucleic acid encoding at least a receptor and/or binding site determining part of a fiber protein of an adenovirus of subgroup D or subgroup F. In a preferred embodiment the invention provides a method for producing said adenovirus vector, comprising welding together, preferably through homologous recombination, two nucleic acid molecules comprising partially overlapping sequences wherein said overlapping sequences allow essentially only one homologous recombination which leads to the generation of a physically linked nucleic acid comprising at least two functional adenovirus inverted terminal repeats, a functional encapsulation signal and a nucleic acid of interest or functional parts, derivatives and/or analogues thereof. In a preferred embodiment at least one of said at least two nucleic acid molecules comprises nucleic acid encoding at least a receptor and/or binding site determining part of a fiber protein of an adenovirus of subgroup D or subgroup F. An important aspect in this embodiment of the invention is that said partially overlapping sequences allow essentially only homologous recombination leading to the generation of a functional adenovirus vector capable of being replicated and packaged into adenovirus particles in the presence of the required transacting functions. With essentially only one is meant that said overlapping sequences in each nucleic acid comprise essentially only one continuous sequence wherein homologous recombination leading to the generation of a functional adenovirus may occur. Within said continuous sequence the actual number of homologous recombination events may be higher than one. Non continuous overlapping sequences are not desired because they reduce the reliability of said method. Non continuous overlapping sequences are also not desired because they reduce the overall efficiency of said method, presumably due to the generation of undesired homologous recombination products.

[0030] A preferred embodiment of the invention provides a method for generating an adenovirus vector wherein both of said nucleic acid molecules comprise only one adenovirus inverted terminal repeat or a functional part, derivative and/or analogue thereof. In one aspect one or both of said two nucleic acid molecules have undergone modifications prior to said welding together. Said modification may include the welding together of different nucleic acid molecules leading to the generation of one or both of said two nucleic acid molecules. In a preferred embodiment said different nucleic acids are welded together through homologous recombination of partially overlapping sequences. In a further aspect said welding together is performed in a cell or a functional part, derivative and/or analogue thereof. Preferably said cell is a mammalian cell. More preferably, said welding together is performed in a cell expressing E1-region encoded proteins. Preferably said cell is a PER.C6 cell (ECACC deposit number 96022940) or a derivative thereof. In a preferred embodiment said nucleic acid molecules are not capable of replicating in said mammalian cell prior to said welding together. Said replication is undesired since it reduces the reliability of the methods of the invention presumably through providing additional targets for undesired homologous recombination. Said replication is also not desired because it reduces the efficiency of the methods of the invention presumably because said replication competes for substrate or adenovirus transacting functions with the replication of said adenovirus vector.

[0031] In a preferred embodiment, one of said nucleic acid molecules is relatively small and the other is relatively large. This configuration is advantageous because it allows easy manipulation of said relatively small nucleic acid molecule allowing for example the generation of a large number of small nucleic acid molecules comprising different nucleic acid of interest for instance for the generation of an adenovirus vector library. Said configuration is also desired because it allows the production of a large batch of quality tested large nucleic acid molecule. The amplification of large nucleic acid molecules for instance in bacteria is difficult in terms of obtaining sufficient amounts of said large nucleic acid. The amplification of large nucleic acid molecules for instance in bacteria is also difficult to control because a small modification of said large nucleic acid is not easily detected. Moreover, for reasons not quite understood some large vectors are more stable in bacteria or yeasts than others. Said configuration however, allows the generation of a standard batch of a large nucleic acid molecule which can be thoroughly tested, for instance through generating a control adenovirus of which the efficiency and the reliability of production is known, and determining said parameters of a new batch of large nucleic acid molecule. Once validated said batch may be used for the generation of a large number of different adenovirus vectors through combining said large molecule with a large number of different small nucleic acid molecules. Said system therefore also allows for the selection and/or manipulation of vectors comprising a large nucleic acid molecule of the invention to allow a suitable yield of intact large nucleic acid.

[0032] In another embodiment said cell comprising nucleic acid encoding E1-region proteins further comprises a

nucleic acid encoding an adenovirus E2-region and/or an adenovirus E4-region protein. Preferably, said cell further comprising nucleic acid encoding an adenovirus E2-region and/or an adenovirus E4-region protein is a derivative of PER.C6.

[0033] In another aspect the invention provides a receptor and/or a binding site for adenoviruses type D and/or F, present on or associated with CAR negative cells. Preferably said receptor and/or a binding site is present on K562 cells, amniotic fluid derived cells and/or primary fibroblast cells.

[0034] In yet another aspect, the invention provides the use of receptor and/or a binding site for adenoviruses type D and/or F, present in and/or on a cell, for the delivery nucleic acid to said cell.

[0035] In yet another embodiment the invention provides the use of a gene delivery vehicle according to anyone of claims 1-14, in a pharmaceutical.

[0036] In another aspect the invention provides a capsid protein derived from a subgroup D and/or a subgroup F adenovirus or a functional part, derivative and/or analogue thereof. Preferably, said protein is a fiber protein. The invention further provides a nucleic acid encoding a capsid protein of the invention. Preferably, said nucleic acid comprises a fiber sequence from a subgroup D and/or a subgroup F as depicted in figure 7.

Detailed description.

[0037] It has been demonstrated in mice that upon *in vivo* systemic delivery of recombinant adenovirus serotype 5 for gene therapy purposes approximately 99% of the virus is trapped in the liver (Herz et al, 1993). Therefore, alteration of the adenovirus serotype 5 host cell range to be able to target other organs *in vivo* is a major interest of the invention.

[0038] The initial step for successful infection is binding of adenovirus to its target cell, a process generally thought to be mediated through fiber protein. The fiber protein has a trimeric structure (Stouten et al, 1992) with different lengths depending on the virus serotype (Signas et al 1985; Kidd et all 1993). Different serotypes have polypeptides with structurally similar N and C termini, but different middle stem regions. N-terminally, the first 30 amino acids are involved in anchoring of the fiber to the penton base (Chroboczek et al, 1995), especially the conserved FNPVYP region in the tail (Arnberg et al 1997). The C-terminus, or knob, is generally thought to be responsible for initial interaction with the cellular adenovirus receptor. After this initial binding secondary binding between the capsid penton base and cell-surface integrins is proposed to lead to internalisation of viral particles in coated pits and endocytosis (Morgan et al, 1969; Svensson et al, 1984; Varga et al, 1992; Greber et al, 1993; Wickham et al, 1994).

[0039] Integrins are $\alpha\beta$ -heterodimers of which at least 14 α -subunits and 8 β -subunits have been identified (Hynes et al, 1992). The array of integrins expressed in cells is complex and will vary between cell types and cellular environment. Although the knob contains some conserved regions, between serotypes, knob proteins show a high degree of variability, indicating that different adenovirus receptors might exist. For instance, it has been demonstrated that adenoviruses of subgroup C (Ad2, Ad5) and adenoviruses of subgroup B (Ad3) bind to different receptors (Defner et al, 1990). By using baculovirus produced soluble CAR as well as adenovirus serotype 5 knob protein, Roelvink et all concluded via interference studies that all adenovirus serotypes, except serotypes of subgroup B, enter cells via CAR (Roelvink et al, 1998). The latter, which is now generally accepted in the field, if valid should thus limit the complexity of using different serotypes for gene therapy purposes.

[0040] Besides the involvement in cell binding, the fiber protein also contains the type specific γ -antigen, which together with the ϵ -antigen of the hexon determines the serotype specificity. The γ -antigen is localised on the fiber and it is known that it consists of 17 amino acids (Elz et al, 1997). The anti-fiber antibodies of the host are therefore directed to the trimeric structure of the knob. To obtain re-directed infection of recombinant adenovirus serotype 5, several approaches have been or still are under investigation. Wickham et al has altered the RGD (Arg, Gly, Asp) motif in the penton base which is believed to be responsible for the $\alpha_v\beta_3$ and $\alpha_v\beta_5$ integrin binding to the penton base. They have replaced this RGD motif by another peptide motif which is specific for the $\alpha_4\beta_1$ receptor. In this way targeting the adenovirus to a specific target cell could be accomplished (Wickham et al, 1995, 1996). Krasnykh et al has made use of the HI loop available in the knob. This loop is, based on X-ray crystallographics, located on the outside of the knob trimeric structure and therefore is thought not to contribute to the intramolecular interactions in the knob (Krasnykh et al, 1998). However, complete CAR independent infection was not observed.

[0041] It is an object of the present invention to provide a method and means by which an adenovirus can infect cells negative for the CAR protein. Therefore, the generation of chimaeric adenoviruses based on adenovirus serotype 5 with a modified fiber gene is described. For this purpose, two or three plasmids, which together contain the complete adenovirus serotype 5 genome, were constructed. From a plasmid the DNA encoding the adenovirus serotype 5 fiber protein was essentially removed and replaced by linker DNA sequences which facilitate easy cloning. This plasmid subsequently served as template for the insertion of DNA encoding for fiber protein derived from different adenovirus serotypes (human or animal). The DNAs derived from the different serotypes were obtained using the polymerase chain reaction technique in combination with (degenerate) oligonucleotides. At the former E1 location in the genome of adenovirus serotype 5, any gene of interest can be cloned. A single transfection procedure of the two or three

plasmids together resulted in the formation of a recombinant chimaeric adenovirus. Although successful introduction of changes in the adenovirus serotype 5 fiber and penton-base have been reported, the complex structure of knob and the limited knowledge of the precise amino acids interacting with CAR render such targeting approaches laborious and difficult. To overcome the limitations described above we used pre-existing adenovirus fibers to maximise the chance of obtaining recombinant adenovirus which can normally assemble in the nucleus of a producer cell and which can be produced on pre-existing packaging cells. By generating a chimaeric adenovirus serotype 5 based fiber library containing fiber proteins of all other human adenovirus serotypes, we have developed a technology which enables rapid screening for a recombinant adenoviral vector with preferred infection characteristics.

[0042] In one aspect this invention describes chimaeric adenoviruses and methods to generate these viruses that have an tropism different from that of adenovirus serotype 5. This chimaeric adenovirus serotype 5 is able to infect cell types which do not express the CAR protein much more efficiently both *in vitro* and *in vivo* than the adenovirus serotype 5. Such cells include but are not limited to endothelial cells, smooth muscle cells, dendritic cells, neuronal cells, glial cells, synovical cells, primary fibroblasts, cells from the amniotic fluid, hemopoietic stem cells, and monocytic/macrophage cells etc.

[0043] In another aspect the invention describes the construction and use of plasmids consisting of distinct parts of adenovirus serotype 5 in which the gene encoding for fiber protein has been replaced with DNA derived from alternative human or animal serotypes. This set of constructs, in total encompassing the complete adenovirus genome, allows for the construction of unique chimaeric adenoviruses customised for transduction of particular cell types or organ(s).

[0044] In all aspects of the invention the chimaeric adenoviruses may, or may not, contain deletions in the E1 region and insertions of heterologous genes linked either or not to a promoter. Furthermore, chimaeric adenoviruses may, or may not, contain deletions in the E3 region and insertions of heterologous genes linked to a promoter. Furthermore, chimaeric adenoviruses may, or may not, contain deletions in the E2 and/ or E4 region and insertions of heterologous genes linked to a promoter. In the latter case E2 and/ or E4 complementing cell lines are required to generated recombinant adenoviruses.

Example 1: Generation of adenovirus serotype 5 genomic plasmid clones

[0045] The complete genome of adenovirus serotype 5 has been cloned into various plasmids or cosmids to allow easy modification of parts of the adenovirus serotype 5 genome, while still retaining the capability to produce recombinant virus. For this purpose the following plasmids were generated:

1. pBr/Ad.Bam-rlTR (ECACC deposit P97082122)

[0046] In order to facilitate blunt end cloning of the ITR sequences, wild-type human adenovirus type 5 (Ad5) DNA was treated with Klenow enzyme in the presence of excess dNTPs. After inactivation of the Klenow enzyme and purification by phenol/chloroform extraction followed by ethanol precipitation, the DNA was digested with BamHI. This DNA preparation was used without further purification in a ligation reaction with pBr322 derived vector DNA prepared as follows: pBr322 DNA was digested with EcoRV and BamHI, dephosphorylated by treatment with TSAP enzyme (Life Technologies) and purified on LMP agarose gel (SeaPlaque GTG). After transformation into competent *E.coli* DH5a (Life Techn.) and analysis of ampicilline resistant colonies, one clone was selected that showed a digestion pattern as expected for an insert extending from the BamHI site in Ad5 to the right ITR. Sequence analysis of the cloning border at the right ITR revealed that the most 3' G residue of the ITR was missing, the remainder of the ITR was found to be correct. Said missing G residue is complemented by the other ITR during replication.

2. pBr/Ad.Sal-rlTR (ECACC deposit P97082119)

[0047] pBr/Ad.Bam-rlTR was digested with BamHI and SalI. The vector fragment including the adenovirus insert was isolated in LMP agarose (SeaPlaque GTG) and ligated to a 4.8 kb SalI-BamHI fragment obtained from wt Ad5 DNA and purified with the Geneclean II kit (Bio 101, Inc.). One clone was chosen and the integrity of the Ad5 sequences was determined by restriction enzyme analysis. Clone pBr/Ad.Sal-rlTR contains adeno type 5 sequences from the SalI site at bp 16746 up to and including the rITR (missing the most 3' G residue).

3. pBr/Ad.Cla-Bam (ECACC deposit P97082117)

[0048] wt Adeno type 5 DNA was digested with ClaI and BamHI, and the 20.6 kb fragment was isolated from gel by electro-elution. pBr322 was digested with the same enzymes and purified from agarose gel by Geneclean. Both fragments were ligated and transformed into competent DH5a. The resulting clone pBr/Ad.Cla-Bam was analysed by re-

restriction enzyme digestion and shown to contain an insert with adenovirus sequences from bp 919 to 21566.

4. pBr/Ad.AfIII-Bam (ECACC deposit P97082114)

5 [0049] Clone pBr/Ad.Cla-Bam was linearised with EcoRI (in pBr322) and partially digested with AfIII. After heat inactivation of AfIII for 20' at 65°C the fragment ends were filled in with Klenow enzyme. The DNA was then ligated to a blunt double stranded oligo linker containing a Pacl site (5'-AATTGTCTTAATTAACCGCTTAA-3'). This linker was made by annealing the following two oligonucleotides: 5'-AATTGTCTTAATTAACCGC-3' and 5'-AATTGCGGTTAACAGAC-3', followed by blunting with Klenow enzyme. After precipitation of the ligated DNA to change buffer, the ligations were digested with an excess Pacl enzyme to remove concatameres of the oligo. The 22016 bp partial fragment containing Ad5 sequences from bp 3534 up to 21566 and the vector sequences, was isolated in LMP agarose (SeaPlaque GTG), religated and transformed into competent DH5a. One clone that was found to contain the Pacl site and that had retained the large adeno fragment was selected and sequenced at the 5' end to verify correct insertion of the Pacl linker in the (lost) AfIII site.

10 15 5. pBr/Ad.Bam-rITRpac#2 (ECACC deposit P97082120) and pBr/Ad.Sam-rITR#8 (ECACC deposit P97082121)

20 [0050] To allow insertion of a Pacl site near the ITR of Ad5 in clone pBr/Ad.Bam-rITR about 190 nucleotides were removed between the ClaI site in the pBr322 backbone and the start of the ITR sequences. This was done as follows: pBr/Ad.Bam-rITR was digested with ClaI and treated with nuclease Bal31 for varying lengths of time (2', 5', 10' and 15'). The extent of nucleotide removal was followed by separate reactions on pBr322 DNA (also digested at the ClaI site), using identical buffers and conditions. Bal31 enzyme was inactivated by incubation at 75°C for 10 minutes, the DNA was precipitated and resuspended in a smaller volume of TE buffer. To ensure blunt ends, DNAs were further treated with T4 DNA polymerase in the presence of excess dNTPs. After digestion of the (control) pBr322 DNA with Sall, satisfactory degradation (~150 bp) was observed in the samples treated for 10' or 15'. The 10' or 15' treated pBr/Ad.Bam-rITR samples were then ligated to the above described blunted Pacl linkers (See pBr/Ad.AfIII-Bam). Ligations were purified by precipitation, digested with excess Pacl and separated from the linkers on an LMP agarose gel. After religation, DNAs were transformed into competent DH5a and colonies analysed. Ten clones were selected that showed a deletion of approximately the desired length and these were further analysed by T-track sequencing (T7 sequencing kit, Pharmacia Biotech). Two clones were found with the Pacl linker inserted just downstream of the rITR. After digestion with Pacl, clone #2 has 28 bp and clone #8 has 27 bp attached to the ITR.

pWE/Ad.AfIII-rITR (ECACC deposit P97082116)

35 [0051] Cosmid vector pWE15 (Clontech) was used to clone larger Ad5 inserts. First, a linker containing a unique Pacl site was inserted in the EcoRI sites of pWE15 creating pWE.pac. To this end, the double stranded Pacl oligo as described for pBr/Ad.AfIII-BamHI was used but now with its EcoRI protruding ends. The following fragments were then isolated by electro-elution from agarose gel: pWE.pac digested with Pacl, pBr/AfIII-Bam digested with Pacl and BamHI and pBr/Ad.Bam-rITR#2 digested with BamHI and Pacl. These fragments were ligated together and packaged using 40 1 phage packaging extracts (Stratagene) according to the manufacturers protocol. After infection into host bacteria, colonies were grown on plates and analysed for presence of the complete insert. pWE/Ad.AfIII-rITR contains all adenovirus type 5 sequences from bp 3534 (AfIII site) up to and including the right ITR (missing the most 3' G residue).

pBr/Ad.IITR-Sal(9.4) (ECACC deposit P97082115)

45 [0052] Adeno 5 wt DNA was treated with Klenow enzyme in the presence of excess dNTPs and subsequently digested with Sall. Two of the resulting fragments, designated left ITR-Sal(9.4) and Sal(16.7)-right ITR, respectively, were isolated in LMP agarose (Seaplaque GTG). pBr322 DNA was digested with EcoRV and Sall and treated with phosphatase (Life Technologies). The vector fragment was isolated using the Geneclean method (BIO 101, Inc.) and ligated to the Ad5 Sall fragments. Only the ligation with the 9.4 kb fragment gave colonies with an insert. After analysis and sequencing of the cloning border a clone was chosen that contained the full ITR sequence and extended to the Sall site at bp 9462.

pBr/Ad.IITR-Sal(16.7) (ECACC deposit P97082118)

55 [0053] pBr/Ad.IITR-Sal(9.4) is digested with Sall and dephosphorylated (TSAP, Life Technologies). To extend this clone up to the third Sall site in Ad5, pBr/Ad.Cla-Bam was linearised with BamHI and partially digested with Sall. A 7.3 kb Sall fragment containing adenovirus sequences from 9462-16746 was isolated in LMP agarose gel and ligated to

the Sall-digested pBr/Ad.IITR-Sal (9.4) vector fragment.

pWE/Ad.AfIII-EcoRI

- 5 [0054] pWE.pac was digested with Clal and 5' protruding ends were filled using Klenow enzyme. The DNA was then
digested with PacI and isolated from agarose gel. pWE/AfIII-rITR was digested with EcoRI and after treatment with
Klenow enzyme digested with PacI. The large 24 kb fragment containing the adenoviral sequences was isolated from
agarose gel and ligated to the Clal-digested and blunted pWE.pac vector using the Ligation Express™ kit from Clontech.
After transformation of Ultracompetent XL10-Gold cells from Stratagene, clones were identified that contained the
10 expected insert. pWE/AfIII-EcoRI contains Ad5 sequences from bp 3534-27336.

Construction of new adapter plasmids

- 15 [0055] The absence of sequence overlap between the recombinant adenovirus and E1 sequences in the packaging
cell line is essential for safe, RCA-free generation and propagation of new recombinant viruses. The adapter plasmid
pMLP1.TK (figure. 1) is an example of an adapter plasmid designed for use according to the invention in combination
with the improved packaging cell lines of the invention. This plasmid was used as the starting material to make a new
vector in which nucleic acid molecules comprising specific promoter and gene sequences can be easily exchanged.

- 20 [0056] First, a PCR fragment was generated from pZipΔMo+PyF101(N') template DNA (described in PCT/
NL96/00195) with the following primers: LTR-1: 5'-CTG TAC GTACCA GTG CAC TGG CCT AGG CAT GGA AAA ATA
CAT AAC TG-3' and LTR-2: 5'-GCG GAT CCT TCG AAC CAT GGT AAG CTT GGT ACC GCT AGC GTT AAC CGG
GCG ACT CAG TCA ATC G-3'. Pwo DNA polymerase (Boehringer Mannheim) was used according to manufacturers
protocol with the following temperature cycles: once 5' at 95°C; 3' at 55°C; and 1' at 72°C, and 30 cycles of 1' at 95°C,
1' at 60°C, 1' at 72°C, followed by once 10' at 72°C. The PCR product was then digested with BamHI and ligated into
25 pMLP10 (Levrero *et al.*, 1991) vector digested with Pvull and BamHI, thereby generating vector pLTR10. This vector
contains adenoviral sequences from bp 1 up to bp 454 followed by a promoter consisting of a part of the Mo-MuLV
LTR having its wild-type enhancer sequences replaced by the enhancer from a mutant polyoma virus (PyF101). The
promoter fragment was designated L420. Next, the coding region of the murine HSA gene was inserted. pLTR10 was
digested with BstBI followed by Klenow treatment and digestion with Ncol. The HSA gene was obtained by PCR am-
plification on pUC18-HSA (Kay *et al.*, 1990) using the following primers: HSA1, 5'-GCG CCA CCA TGG GCA GAG
30 CGA TGG TGG C-3' and HSA2, 5'-GTT AGA TCT AAG CTT GTC GAC ATC GAT CTA CTA ACA GTA GAG ATG TAG
AA-3'. The 269 bp amplified fragment was subcloned in a shuttle vector using the Ncol and BgIII sites. Sequencing
confirmed incorporation of the correct coding sequence of the HSA gene, but with an extra TAG insertion directly
35 following the TAG stop codon. The coding region of the HSA gene, including the TAG duplication was then excised as
a Ncol (sticky)-Sall (blunt) fragment and cloned into the 3.5 kb Ncol(sticky)/BstBI(blunt) fragment from pLTR10, result-
ing in pLTR-HSA10.

- Finally, pLTR-HSA10 was digested with EcoRI and BamHI after which the fragment containing the left ITR, packaging
signal, L420 promoter and HSA gene was inserted into vector pMLP1.TK digested with the same enzymes and thereby
40 replacing the promoter and gene sequences. This resulted in the new adapter plasmid pAd/L420-HSA (figure. 2) that
contains convenient recognition sites for various restriction enzymes around the promoter and gene sequences. SnaBI
and AvrII can be combined with HpaI, NheI, KpnI, HindIII to exchange promoter sequences, while the latter sites can
be combined with the Clal or BamHI sites 3' from HSA coding region to replace genes in this construct.

- Another adapter plasmid that was designed to allow easy exchange of nucleic acid molecules was made by replacing
the promoter, gene and poly A sequences in pAd/L420-HSA with the CMV promoter, a multiple cloning site, an intron
45 and a poly-A signal. For this purpose, pAd/L420-HSA was digested with AvrII and BgIII followed by treatment with
Klenow to obtain blunt ends. The 5.1 kb fragment with pBR322 vector and adenoviral sequences was isolated and
ligated to a blunt 1570 bp fragment from pcDNA1/amp (Invitrogen) obtained by digestion with Hhal and AvrII followed
by treatment with T4 DNA polymerase. This adapter plasmid was named pCLIP (figure. 3).

50 Generation of recombinant adenoviruses

- [0057] To generate E1 deleted recombinant adenoviruses with the new plasmid-based system, the following constructs are prepared:

- 55 a) An adapter construct containing the expression cassette with the gene of interest linearised with a restriction
enzyme that cuts at the 3' side of the overlapping adenoviral genome fragment, preferably not containing any
pBR322 vector sequences, and
b) A complementing adenoviral genome construct pWE/Ad.AfIII-rITR digested with PacI.

These two DNA molecules are further purified by phenol/ chloroform extraction and EtOH precipitation. Co-transfection of these plasmids into an adenovirus packaging cell line, preferably a cell line according to the invention, generates recombinant replication deficient adenoviruses by a one-step homologous recombination between the adapter and the complementing construct (figure. 4).

5 Alternatively, in stead of pWE/Ad.AfIII-rITR other fragments can be used, e.g., pBr/Ad.Cla-Bam digested with EcoRI and BamHI or pBr/Ad.AfIII-BamHI digested with Pael and BamHI can be combined with pBr/Ad.Sal-rITR digested with SalI. In this case, three plasmids are combined and two homologous recombinations are needed to obtain a recombinant adenovirus (figure. 5). It is to be understood that those skilled in the art may use other combinations of adapter and complementing plasmids without departing from the present invention. A general protocol as outlined below and
10 meant as a nonlimiting example of the present invention has been performed to produce several recombinant adenoviruses using various adapter plasmids and the Ad.AfIII-rITR fragment. Adenovirus packaging cells (PER.C6) were seeded in ~25 cm² flasks and the next day when they were at ~80% confluency, transfected with a mixture of DNA and lipofectamine agent (Life Techn.) as described by the manufacturer. Routinely, 40 µl lipofectamine, 4 µg adapter
15 plasmid and 4 µg of the complementing adenovirus genome fragment AfIII- rITR (or 2 µg of all three plasmids for the double homologous recombination) are used. Under these conditions transient transfection efficiencies of ~50% (48 hrs post transfection) are obtained as determined with control transfections using a pAd/CMV-LacZ adapter. Two days later, cells are passaged to ~ 80 cm² flasks and further cultured. Approximately five (for the single homologous recombination) to eleven days (for the double homologous recombination) later a cytopathogenic effect (CPE) is seen, indicating that functional adenovirus has formed. Cells and medium are harvested upon full CPE and recombinant virus
20 is released by freeze-thawing. An extra amplification step in an 80 cm² flask is routinely performed to increase the yield since at the initial stage the titers are found to be variable despite the occurrence of full CPE. After amplification, viruses are harvested and plaque purified on PER.C6 cells. Individual plaques are tested for viruses with active transgenes.

25 [0058] Besides replacements in the E1 region it is possible to delete or replace (part of) the E3 region in the adenovirus because E3 functions are not necessary for the replication, packaging and infection of the (recombinant) virus. This creates the opportunity to use a larger insert or to insert more than one gene without exceeding the maximum package size (approximately 105% of wt genome length). This can be done, e.g., by deleting part of the E3 region in the pBr/ Ad.Bam-rITR clone by digestion with XbaI and religation. This removes Ad5 wt sequences 28592-30470 including all known E3 coding regions. Another example is the precise replacement of the coding region of gp19K in the E3 region
30 with a polylinker allowing insertion of new sequences. This, 1) leaves all other coding regions intact and 2) obviates the need for a heterologous promoter since the transgene is driven by the E3 promoter and pA sequences, leaving more space for coding sequences.

To this end, the 2.7 kb EcoRI fragment from wt Ad5 containing the 5' part of the E3 region was cloned into the EcoRI site of pBluescript (KS⁺) (Stratagene). Next, the HindIII site in the polylinker was removed by digestion with EcoRV and HincII and subsequent religation. The resulting clone pBS.Eco-Eco/ad5DHIII was used to delete the gp19K coding region. Primers 1 (5'-GGG TAT TAG GCC AA AGG CGC A-3') and 2 (5'-GAT CCC ATG GAA GCT TGG GTG GCG ACC CCA GCG-3') were used to amplify a sequence from pBS.Eco-Eco/Ad5DHIII corresponding to sequences 28511 to 28734 in wt Ad5 DNA. Primers 3 (5'-GAT CCC ATG GGG ATC CTT TAC TAA GTT ACA AAG CTA-3') and 4 (5'-GTC GCT GTA GTT GGA CTG G-3') were used on the same DNA to amplify Ad5 sequences from 29217 to 29476. The
40 two resulting PCR fragments were ligated together by virtue of the new introduced Ncol site and subsequently digested with XbaI and MunI. This fragment was then ligated into the pBS.Eco-Eco/ad5ΔHIII vector that was digested with XbaI (partially) and MunI generating pBS.Eco-Eco/ad5ΔHIII.Δgp19K. To allow insertion of foreign genes into the HindIII and BamHI site, an XbaI deletion was made in pBS.Eco-Eco/ad5ΔHIII.Δgp19K to remove the BamHI site in the Bluescript polylinker. The resulting plasmid pBS.Eco-Eco/ad5ΔHIII.Δgp19KΔXbaI, contains unique HindIII and BamHI sites corresponding to sequences 28733 (HindIII) and 29218 (BamHI) in Ad5. After introduction of a foreign gene into these sites, either the deleted XbaI fragment is re-introduced, or the insert is recloned into pBS.Eco-Eco/ad5ΔHIII.Δgp19K using HindIII and for example MunI. Using this procedure, we have generated plasmids expressing HSV-TK, hIL-1a, rat IL-3, luciferase or LacZ. The unique SrfI and NotI sites in the pBS.Eco-Eco/ad5ΔHIII.Δgp19K plasmid (with or without inserted gene of interest) are used to transfer the region comprising the gene of interest into the corresponding region
45 of pBr/Ad.Bam-rITR, yielding construct pBr/Ad.Bam-rITRΔgp19K (with or without inserted gene of interest). This construct is used as described *supra* to produce recombinant adenoviruses. In the viral context, expression of inserted genes is driven by the adenovirus E3 promoter.
50 [0059] Recombinant viruses that are both E1 and E3 deleted are generated by a double homologous recombination procedure as described above for E1-replacement vectors using a plasmid-based system consisting of:

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- a) an adapter plasmid for E1 replacement according to the invention, with or without insertion of a first gene of interest,
- b) the pWE/Ad.AfIII-EcoRI fragment, and

c) the pBr/Ad.Bam-rITR Δ gp19K plasmid with or without insertion of a second gene of interest.

In addition to manipulations in the E3 region, changes of (parts of) the E4 region can be accomplished easily in pBr/Ad.Bam-rITR. Generation and propagation of such a virus, however, in some cases demands complementation *in trans*.

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Example 2: Generation of adenovirus serotype 5 based viruses with chimaeric fiber proteins

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[0060] The method described *infra* to generate recombinant adenoviruses by co-transfection of two, or more separate cloned adenovirus sequences. One of these cloned adenovirus sequences was modified such that the adenovirus serotype 5 fiber DNA was deleted and substituted for unique restriction sites thereby generating template clones which allow for the easy introduction of DNA sequences encoding for fiber protein derived from other adenovirus serotypes.

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Generation of adenovirus template clones lacking DNA encoding for fiber

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[0061] The fiber coding sequence of adenovirus serotype 5 is located between nucleotides 31042 and 32787. To remove the adenovirus serotype 5 DNA encoding fiber we started with construct pBr/Ad.Bam-rITR. First a NdeI site was removed from this construct. For this purpose, pBR322 plasmid DNA was digested with NdeI after which protruding ends were filled using Klenow enzyme. This pBR322 plasmid was then re-ligated, digested with NdeI and transformed into *E.coli* DH5 α . The obtained pBr/ Δ NdeI plasmid was digested with ScaI and Sall and the resulting 3198 bp vector fragment was ligated to the 15349 bp ScaI-Sall fragment derived from pBr/Ad.BamrITR, resulting in plasmid pBr/Ad.Bam-rITR Δ NdeI which hence contained a unique NdeI site. Next a PCR was performed with oligonucleotides NY-up: 5'- CGA CAT ATG TAG ATG CAT TAG TTT GTG TTA TGT TTC AAC GTG-3'

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And NY-down: 5'-GGA GAC CAC TGC CAT GTT-3' (figure 6). During amplification, both a NdeI (bold face) and a NsiI restriction site (underlined) were introduced to facilitate cloning of the amplified fiber DNAs. Amplification consisted of 25 cycles of each 45 sec. at 94°C, 1 min. at 60°C, and 45 sec. at 72°C. The PCR reaction contained 25 pmol of oligonucleotides NY-up or NY-down, 2mM dNTP, PCR buffer with 1.5 mM MgCl₂, and 1 unit of Elongase heat stable polymerase (Gibco, The Netherlands). One-tenth of the PCR product was run on an agarose gel which demonstrated that the expected DNA fragment of \pm 2200 bp was amplified. This PCR fragment was subsequently purified using Geneclean kit system (Bio101 Inc.). Then, both the construct pBr/Ad.Bam-rITR Δ NdeI as well as the PCR product were digested with restriction enzymes NdeI and SbfI. The PCR fragment was subsequently cloned using T4 ligase enzyme into the NdeI and SbfI digested pBr/Ad.Bam-rITR Δ NdeI, generating pBr/Ad.BamR Δ Fib. This plasmid allows insertion of any PCR amplified fiber sequence through the unique NdeI and NsiI sites that are inserted in place of the removed fiber sequence. Viruses can be generated by a double homologous recombination in packaging cells described *infra* using an adapter plasmid, construct pBr/Ad.AflII-EcoRI digested with Pael and EcoRI and a pBr/Ad.BamR Δ Fib construct in which heterologous fiber sequences have been inserted. To increase the efficiency of virus generation, the construct pBr/Ad.BamR Δ Fib was modified to generate a Pael site flanking the right ITR. Hereto, pBr/Ad.BamR Δ Fib was digested with AvrII and the 5 kb adeno fragment was isolated and introduced into the vector pBr/Ad.Bam-rITR.pac#8 replacing the corresponding AvrII fragment. The resulting construct was named pBr/Ad.BamR Δ Fib.pac. Once a heterologous fiber sequence is introduced in pBr/Ad.BamR Δ Fib.pac, the fiber modified right hand adenovirus clone may be introduced into a large cosmid clone as described for pWE/Ad.AflII-rITR in example 1. Such a large cosmid clone allows generation of adenovirus by only one homologous recombination making the process extremely efficient.

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Amplification of fiber sequences from adenovirus serotypes

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[0062] To enable amplification of the DNAs encoding fiber protein derived from alternative serotypes degenerate oligonucleotides were synthesised. For this purpose, first known DNA sequences encoding for fiber protein of alternative serotypes were aligned to identify conserved regions in both the tail-region as well as the knob-region of the fiber protein. From the alignment, which contained the nucleotide sequence of 19 different serotypes representing all 6 subgroups, (degenerate) oligonucleotides were synthesised (see table 2). Also shown in table 3 is the combination of oligonucleotides used to amplify the DNA encoding fiber protein of a specific serotype. The amplification reaction (50 μ l) contained 2 mM dNTPs, 25 pmol of each oligonucleotide, standard 1x PCR buffer, 1,5 mM MgCl₂, and 1 Unit Pwo heat stable polymerase (Boehringer) per reaction. The cycler program contained 20 cycles, each consisting of 30 sec. 94°C, 60 sec. 60-64°C, and 120 sec. At 72°C. One-tenth of the PCR product was run on an agarose gel which demonstrated that a DNA fragment was amplified. Of each different template, two independent PCR reactions were performed after which the independent PCR fragments obtained were sequenced to determine the nucleotide sequence. From 11 different serotypes, the nucleotide sequence could be compared to sequences present in Genbank. Of all other serotypes, the DNA encoding fiber protein was previously unknown and was therefore aligned with known se-

quences from other subgroup members to determine homology i.e. sequence divergence. Of the 51 human serotypes known to date, all fiber sequences, except for serotypes 1, 6, and 26, have been amplified and sequenced. The protein sequences of the fiber from different adenovirus serotypes is given in figure 7.

5 Generation of fiber chimaeric adenoviral DNA constructs

[0063] All amplified fiber DNAs as well as the vector (pBr/Ad.BamRΔ Fib) were digested with NdeI and NsiI. The digested DNAs was subsequently run on a agarose gel after which the fragments were isolated from the gel and purified using the Geneclean kit (Bio101 Inc). The PCR fragments were then cloned into the NdeI and NsiI sites of pBr/Ad-BamRAFib, thus generating pBr/AdBamRFibXX (where XX stands for the serotype number of which the fiber DNA was isolated). So far the fiber sequence of serotypes 5/ 7/ 8/ 9/ 10/ 11/ 12/ 13/ 14/ 16/ 17/ 19/ 21/ 24/ 27/ 28/ 29/ 30/ 32/ 33/ 34/ 35/ 36/ 37/ 38/ 40-S/ 40-L/ 41-S/ 42/45/ 47/ 49/ 51 have been cloned into pBr/AdBamRFibXX. From pBr/AdBamRFibXX (where XX is 5/ 8/ 9/ 10/ 11/ 13/ 16/ 17/ 24/ 27/ 30/ 32/ 33/ 34/ 35/ 38/ 40-S/ 40-L/ 45/ 47/ 49/ 51) an 6 kb AvrII fragment encompassing the fiber sequence was isolated via gelectrophoresis and Geneclean. This AvrII fragment was subsequently cloned in plasmid pBr/Ad.Bam-rITR.pac (see example 1) which was digested to completion with AvrII and dephosphorylated as described previously, leading to the generation of the plasmid pBr/Ad.Bam-rITR.pac.fibXX. This plasmid was subsequently used to generate a cosmid clone with a modified fiber using the constructs pWE.pac, pBr/AfIII-Bam and pBr/Ad.Bam-rITR.pac.fibXX. This cosmid cloning resulted in the formation of construct pWE/Ad.AfIII-rITR/FibXX (where XX stands for the serotype number of which the fiber DNA was isolated).

20 Generation of pAd5/L420.HSA, pAd5/Clip and pAd5/Clipsal

[0064] pMLPI.TK was used to make a new vector in which nucleic acid molecules comprising specific promoter and gene sequences can be easily exchanged.

25 First, a PCR fragment was generated from pZipΔMo+PyF101(N⁺) template DNA (described in PCT/NL96/00195) with the following primers: LTR-1: 5'-CTG TAC CCA GTG CAC TGG CCT AGG CAT GGA AAA ATA CAT AAC TG-3' and LTR-2: 5'-GCG GAT CCT TCG AAC CAT GGT AAG CTT GGT ACC GCT AGC GTT AAC CGG GCG ACT CAG TCA ATC G-3'. Pwo DNA polymerase (Boehringer Mannheim) was used according to manufacturers protocol with the following temperature cycles: once 5' at 95°C; 3' at 55°C; and 1' at 72°C, and 30 cycles of 1' at 95°C, 1' at 60°C, 1' at 72°C, followed by once 10' at 72°C. The PCR product was then digested with BamHI and ligated into pMLP10 (Levredo et al., 1991; Gene 101, 195-202) digested with Pvull and BamHI, thereby generating vector pLTR10. This vector contains adenoviral sequences from bp 1 up to bp 454 followed by a promoter consisting of a part of the Mo-MuLV LTR having its wild-type enhancer sequences replaced by the enhancer from a mutant polyoma virus (PyF101). The promoter fragment was designated L420. Sequencing confirmed correct amplification of the LTR fragment however the most 5' bases in the PCR fragment were missing so that the Pvull site was not restored. Next, the coding region of the murine HSA gene was inserted. pLTR10 was digested with BstBI followed by Klenow treatment and digestion with NcoI. The HSA gene was obtained by PCR amplification on pUC18-HSA (Kay et al., 1990; J. Immunol. 145, 1952-1959) using the following primers: HSA1, 5'-GCG CCA CCA TGG GCA GAG CGA TGG TGG C-3' and HSA2, 5'-GTT AGA TCT AAG CTT GTC GAC ATC GAT CTA CTA ACA GTA GAG ATG TAG AA-3'. The 269 bp amplified fragment was 30 subcloned in a shuttle vector using the NcoI and BgIII sites. Sequencing confirmed incorporation of the correct coding sequence of the HSA gene, but with an extra TAG insertion directly following the TAG stop codon. The coding region of the HSA gene, including the TAG duplication was then excised as a NcoI(sticky)-Sall(blunt) fragment and cloned into the 3.5 kb NcoI(sticky)/BstBI(blunt) fragment from pLTR10, resulting in pLTR-HSA10.

35 Finally, pLTR-HSA10 was digested with EcoRI and BamHI after which the fragment containing the left ITR, packaging signal, L420 promoter and HSA gene was inserted into vector pMLPI.TK digested with the same enzymes and thereby replacing the promoter and gene sequences. This resulted in the new adapter plasmid pAd5/L420-HSA that contains convenient recognition sites for various restriction enzymes around the promoter and gene sequences. SnaBI and AvrII can be combined with HpaI, NheI, KpnI, HindIII to exchange promoter sequences, while the latter sites can be combined with the ClaI or BamHI sites 3' from HSA coding region to replace genes in this construct.

40 [0065] Another adapter plasmid that was designed to allow easy exchange of nucleic acid molecules was made by replacing the promoter, gene and polyA sequences in pAd5/L420-HSA with the CMV promoter, a multiple cloning site, an intron and a polyA signal. For this purpose, pAd5/L420-HSA was digested with AvrII and BgIII followed by treatment with Klenow to obtain blunt ends. The 5.1 kb fragment with pBr322 vector and adenoviral sequences was isolated and ligated to a blunt 1570 bp fragment from pcDNA1/amp (Invitrogen) obtained by digestion with HhaI and AvrII followed 45 by treatment with T4 DNA polymerase. This adapter plasmid was named pAd5/Clip. To enable removal of vector sequences from the adenoviral fragment pAd5/Clip was partially digested with EcoRI and the linear fragment was isolated. An oligo of the sequence 5' TTAAGTCGAC-3' was annealed to itself resulting in a linker with a Sall site and EcoRI overhang. The linker was ligated to the partially digested pAd5/Clip vector and clones were selected that had the linker

inserted in the EcoRI site 23 bp upstream of the left adenovirus ITR in pAd5/Clip resulting in pAd5/Clipsal.

Generation of pAd5ClipLacZ, PAd5Clip.Luc, pAd5Clip.TK and pAd5Clipsal.Luc

- 5 [0066] The adapter plasmid pAd5/Clip.LacZ was generated as follows: The E.coli LacZ gene was amplified from the plasmid pMLP.nlsLacZ (EP 95-202 213) by PCR with the primers
 5'GGGGTGGGCCAGGGTACCTCTAGGCTTTGCAA and
 5'GGGGGGATCCATAAACAAAGTCAGAAATCC. The PCR reaction was performed Ex Taq (Takara) according to the suppliers protocol at the following amplification program: 5 minutes 94°C, 1 cycle; 45 seconds 94°C and 30 seconds
 10 60°C and 2 minutes 72°C, 5 cycles; 45 seconds 94°C and 30 seconds 65°C and 2 minutes 72°C, 25 cycles; 10 minutes 72; 45 seconds 94°C and 30 seconds 60°C and 2 minutes 72°C, 5 cycles, 1 cycle. The PCR product was subsequently digested with KpnI and BamHI and the digested DNA fragment was ligated into KpnI/BamHI digested pcDNA3 (Invitrogen), giving rise to pcDNA3.nlsLacZ. Next, the plasmid pAd5/Clip was digested with SpeI. The large fragment containing part of the 5' part CMV promoter and the adenoviral sequences was isolated. The plasmid pcDNA3.nlsLacZ
 15 was digested with SpeI and the fragment containing the 3'part of the CMV promoter and the lacZ gene was isolated. Subsequently, the fragments were ligated, giving rise to pAd/Clip.LacZ. The reconstitution of the CMV promoter was confirmed by restriction digestion.
- [0067] The adapter plasmid pAd5/Clip.Luc was generated as follows: The plasmid pCMV.Luc (EP 95-202 213) was digested with HindIII and BamHI. The DNA fragment containing the luciferase gene was isolated. The adapter plasmid
 20 pAd5/Clip was digested with HindIII and BamHI, and the large fragment was isolated. Next, the isolated DNA fragments were ligated, giving rise to pAd5/Clip.Luc. The adapter pClipsal.Luc was generated in the same way but using the adapter pClipsal digested with HIII and BamHI as vector fragment. Likewise, the TK containing HIII-BamHI fragment from pCMV.TK (EP 95-202 213) was inserted in pClipsal to generate pAd5/Clip.TK. The presence of the Sall site just upstream of the left ITR enables liberation of vector sequences from the adeno insert. Removal of these vector sequences enhances frequency of vector generation during homologous recombination in PER.C6.

Generation of recombinant adenovirus chimaeric for fiber protein

- 30 [0068] To generate recombinant Ad 5 virus carrying the fiber of serotype 12, 16, 28, 40-L, 51, and 5, three constructs, pCLIP.Luc, pWE/AdAfIII-Eco and pBr/AdBamrITR.pac/fibXX (XX = 12, 16, 28, 40-L, 51, and 5) were transfected into adenovirus producer cells. To generate recombinant Ad 5 virus carrying the fiber of 5/ 7/ 8/ 9/ 10/ 11/ 12/ 13/ 14/ 16/ 17/ 19/ 21/ 24/ 27/ 28/ 29/ 30/ 32/ 33/ 34/ 35/ 36/ 37/ 38/ 40-S/ 40-L/ 41-S/ 42/45/ 47/ 49/ 51, two constructs pCLIP.Luc and pWE/Ad.AfIII-rlTR/FibXX were transfected into adenovirus producer cells. For transfection, 2 µg of pCLIP.Luc, and 4 µg of both pWE/AdAfIII-Eco and pBr/AdBamrITR.pac/fibXX (or in case of cosmids: 4 µg of pCLIP.Luc plus 4 µg of pWE/Ad.AfIII-rlTR/FibXX) were diluted in serum free DMEM to 100 µl total volume. To this DNA suspension 100 µl 1x diluted lipofectamine (Gibco) was added. After 30 minutes at room temperature the DNA-lipofectamine complex solution was added to 2.5 ml of serum-free DMEM which was subsequently added to a T25 cm² tissue culture flask. This flask contained 2x10⁶ PER.C6 cells that were seeded 24-hours prior to transfection. Two hours later, the DNA-lipofectamine complex containing medium was diluted once by the addition of 45
 40 2.5 ml DMEM supplemented with 20% foetal calf serum. Again 24 hours later the medium was replaced by fresh DMEM supplemented with 10% foetal calf serum. Cells were cultured for 6-8 days, subsequently harvested, and freeze/thawed 3 times. Cellular debris was removed by centrifugation for 5 minutes at 3000 rpm room temperature. Of the supernatant (12.5 ml) 3-5 ml was used to infect again infect PER.C6 cells (T80 cm² tissue culture flasks). This re-infection results in full cytopathogenic effect (CPE) after 5-6 days after which the adenovirus is harvested as described above.

Example 3: Production, purification, and titration of fiber chimaeric adenoviruses

- 50 [0069] Of the supernatant obtained from transfected PER.C6 cells typically 10 ml was used to inoculate a 1 litre fermentor which contained 1 - 1.5 x 10⁸ cells/ ml PER.C6 that were specifically adapted to grow in suspension. Three days after inoculation, the cells were harvested and pelleted by centrifuging for 10 min at 1750 rpm at room temperature. The chimaeric adenoviruses present in the pelleted cells were subsequently extracted and purified using the following downstream processing protocol. The pellet was dissolved in 50 ml 10 mM NaPO₄⁻ and frozen at -20°C. After thawing at 37°C, 5.6 ml deoxycholate (5% w/v) was added after which the solution was homogenated. The solution was subsequently incubated for 15 minutes at 37°C to completely crack the cells. After homogenising the solution, 1875 µl (1M) MgCl₂ was added and 5 ml 100% glycerol. After the addition of 375 µl DNase (10 mg/ ml) the solution was incubated for 30 minutes at 37°C. Cell debris was removed by centrifugation at 1880xg for 30 minutes at room temperature without the brake on. The supernatant was subsequently purified from proteins by loading on 10 ml of freon. Upon centrifugation for 15 minutes at 2000 rpm without brake at room temperature three bands are visible of which

the upper band represents the adenovirus. This band was isolated by pipetting after which it was loaded on a Tris/HCl (1M) buffered caesiumchloride blockgradient (range: 1.2 to 1.4 gr./ml). Upon centrifugation at 21000 rpm for 2.5 hours at 10°C the virus was purified from remaining protein and cell debris since the virus, in contrast to the other components, does not migrate into the 1.4 gr./ ml caesiumchloride solution. The virus band is isolated after which a second purification using a Tris/ HCl (1M) buffered continues gradient of 1.33 gr./ml of caesiumchloride is performed. After virus loading on top of this gradient the virus is centrifuged for 17 hours at 55000 rpm at 10°C. Subsequently the virus band is isolated and after the addition of 30 µl of sucrose (50 w/v) excess caesiumchloride is removed by three rounds of dialysis, each round comprising of 1 hour. For dialysis the virus is transferred to dialysis slides (Slide-a-lizer, cut off 10000 kDa, Pierce, USA). The buffers used for dialysis are PBS which are supplemented with an increasing concentration of sucrose (round 1 to 3: 30 ml, 60 ml, and 150 ml sucrose (50% w/v)/ 1.5 litre PBS, all supplemented with 7.5 ml 2% (w/v) CaMgCl₂). After dialysis, the virus is removed from the slide-a-lizer after which it is aliquoted in portions of 25 and 100 µl upon which the virus is stored at -85°C.

[0070] To determine the number of virus particles per millilitre, 100 µl of the virus batch is run on an high pressure liquid chromatograph (HPLC). The adenovirus is bound to the column (anion exchange) after which it is eluted using a NaCl gradient (range 300-600 mM). By determining the area under the virus peak the number of virus particles can be calculated. To determine the number of infectious units (IU) per ml present in a virus batch, titrations are performed on 911 cells. For this purpose, 4x10⁴ 911 cells are seeded per well of 96-well plates in rows B, D, and F in a total volume of 100 µl per well. Three hours after seeding the cells are attached to the plastic support after which the medium can be removed. To the cells a volume of 200 µl is added, in duplicate, containing different dilutions of virus (range: 10² times diluted to 2x10⁹). By screening for CPE the highest virus dilution which still renders CPE after 14 days is considered to contain at least one infectious unit. Using this observation, together with the calculated amount of virus volume present in these wells renders the number of infectious units per ml of a given virus batch. The production results i.e. virus particles per ml and IU per ml or those chimaeric adenoviruses that were produced so far, are shown in table 3.

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Example 4: Presence of Ad5 Receptor molecules on human cells

[0071] To investigate the importance of the presence of CAR on target cells for infection with chimaeric adenoviruses, a panel of human cell lines and primary cells were tested for the presence and/ or absence of CAR, MHC class I, and integrins (α v β 3, α v β 5). For this purpose, 1x10⁵ target cells or were transferred to tubes (4 tubes per cell type) designed for flow cytometry. Cells were washed once with PBS/ 0.5% BSA after which the cells were pelleted by centrifugation for 5 minutes at 1750 rpm at room temperature. Subsequently, 10 µl of a 100 times diluted α , β 3 antibody (Mab 1961, Brunswick chemie, Amsterdam, The Netherlands), a 100 times diluted antibody α , β 5 (antibody (Mab 1976, Brunswick chemie, Amsterdam, The Netherlands), or 2000 times diluted CAR antibody was a kind gift of Dr. Bergelson, Harvard Medical School, Boston, USA (Hsu et al) was added to the cell pellet after which the cells were incubated for 30 minutes at 4°C in a dark environment. After this incubation, cells were washed twice with PBS/0.5% BSA and again pelleted by centrifugation for 5 minutes at 1750 rpm room temperature. To label the cells, 10 µl of rat anti mouse IgG1 labelled with phycoerythrin (PE) was added to the cell pellet upon which the cells were again incubated for 30 minutes at 4°C in a dark environment. Finally the cells were washed twice with PBS/0.5% BSA and analysed on a flow cytometer. The results of flow cytometric analysis of these experiments are shown in table 4. These results show that human erythroid leukemia cells (K562, ATCC: CCL-243), human primary fibroblasts (GM09503), human primary smooth muscle cells, and primary human synoviocytes do not express detectable levels of the CAR receptor. In contrast, human lung carcinoma cells (A549, ATCC: CCL-1185), human lymphoblast cells (SupT1 (B and T cell hybrid, ATCC, CRL-1991), and human liver cells (HEPG2, ATCC, HB8065) express high amounts of CAR protein. Human lymphoblast cells (CEM, ATCC: CRL-1992), primary human umbilical vein endothelial cells (HUVEC), and human primary chorion villi express low amounts of CAR protein.

Example 5: Infection of CAR negative cells with fiber chimaeric adenovirus

[0072] Several of the cell types described in example 4, i.e. A549, K562, GM09503, SupT1, chorion villi, and HepG2 were infected with a panel of chimaeric adenoviruses. This panel consists of adenovirus serotype 5 (subgroup C), and of adenovirus serotype 5 containing the fiber of serotypes 16 and 51 (subgroup B), of 28, 32, and 49 (subgroup D), of 12 (subgroup A), and of 40 (40-S and/or 40-L: subgroup F). For this purpose target cells are seeded at a concentration of 10⁵ cells per well of 6-well plates in 2 ml Dulbecco's modified Eagles medium (DMEM, Life Technologies, The Netherlands) supplemented with 10% Foetal calf serum. Twenty-four hours later the medium is replaced by fresh medium containing the different chimaeric adenoviruses at an increasing MOI of 0, 10, 50, 250, 1250, 2500, 5000 (MOI based on virus particles per millilitre). Approximately 2 hours after the addition of virus the medium containing the virus is discarded, cells are washed once with PBS, and subsequently 2 ml of fresh medium (not containing virus) is added

to each well. Forty-eight hours later cells are harvested, washed and pelleted by centrifuging 5 minutes at 1500 rpm. Cells are subsequently lysed in 0,1 ml lysis buffer (1% Triton-X-100, 15% Glycerol, 2 mM EDTA, 2 mM DTT, and 25 mM MgCl₂ in Tris-phosphate buffer pH 7.8) after which the total protein concentration of the lysate is measured (Biorad, protein standard II). To determine marker gene expression (luciferase activity) 20 µl of the protein sample is mixed with 5 100 µl of a luciferase substrate (Luciferine, Promega, The Netherlands) and subsequently measured on a Lumat LB 9507 apparatus (EG & G Berthold, The Netherlands). The results of these infection experiments, given as the amount of luciferase activity (RLU) per µg protein, are shown in figures 8-14. From these infection experiments several conclusions can be drawn. The infection of A549 cells (figure 8) demonstrates that all chimaeric adenoviruses tested infect with relative high efficiency these cells. The infection of K562 cells (figure 9) demonstrates that these cells cannot be 10 transduced with adenovirus serotype 5 (subgroup C) or the fiber chimera 12 (subgroup A). All other chimaeric adenoviruses (16/51: subgroup B; 28/32/49: subgroup D; 40-L: subgroup F) are able to infect these cells with different efficiencies. The infection of GM09503 primary human fibroblasts (figure 10) demonstrates that these cells can be transduced with all fiber chimeras including Adenovirus serotype 5 albeit with different efficiencies. The infection of SupT1 cells (figure 11) demonstrates that these cells can be transduced with all fiber chimeras albeit with different 15 efficiencies except for fiber chimera 49 which does not infect these human lymphoblast cells. The infection of human chorion villi cells (figure 12) shows a similar transduction pattern as observed with K562 cells except for adenovirus chimera 49 which does not infect these cells. The infection of HEPG2 cells (figure 13) shows a similar transduction pattern as observed with A549 cells. Linking the CAR expression data of these cells to the infection efficiency data obtained, several conclusions can be drawn. 1) Infection of adenovirus serotype 5 is correlated with the presence of 20 CAR (figure 8-13). 2) In the absence of CAR but in the presence of high amount of MHC class I, poor infection is observed using adenovirus serotype 5, indicating that MHC class I is a worse receptor for adenovirus serotype 5 as compared to CAR (figure 10). 3) In the absence of CAR adenovirus fiber chimeras 16 and 51 (subgroup B) as well as chimeras 28 and 32 (subgroup D) as well as chimera 40-L (subgroup F) can infect cells with high efficiency, indicating that these viruses can utilise receptors other than CAR (figures 9 and 12). 4) A comparison of the infection data of the 25 chimaeric adenoviruses carrying the fiber of 28, 32, and 49 teaches that within an adenovirus subgroup differences in transduction efficiencies exist, indicating that adenovirus members of one subgroup either have different affinities for the same receptor, or that different adherence molecules can be used (figures 8-13) by members of an adenovirus subgroup.

30 Example 6: Complexity of receptor recognition of adenovirus serotypes

[0073] To investigate the complexity and/or the number of different adherence molecules which can be used by human adenoviruses from different subgroups or between members within one subgroup the following strategies are designed.

35 1) Interference studies with total chimaeric viruses

[0074] Via infection experiments described in example 5, cell lines are identified that are poorly transducible with a chimaeric viruses carrying the fiber protein of for example serotype 49 (subgroup D) indicating that such a cell expresses 40 low levels of the adherence molecule required for D group adenovirus infection. Next, chimaeric adenoviruses carrying the fiber protein of other members of subgroup D are mixed in different concentrations with the fiber 49 chimaeric adenovirus and subsequently added to the cells. Since the fiber 49 chimaeric adenovirus carries a transgene other than the other subgroup D chimaeric adenoviruses (including but not limited to LacZ, Green Fluorescent Protein Yellow Fluorescent Protein, Luciferase etc) interference of infection can be visualised. As a positive control two fiber 49 chimaeric adenoviruses carrying different marker genes is used. Identical to the example for subgroup D described above 45 experiments are conducted with different members of subgroup A, B, C, E, and F. These experiments show if the fiber protein of members of the same adenovirus subgroup recognise the same adherence molecules on a cell membrane. Naturally, this approach is also used to investigate inter-subgroup variation for example usage of adherence molecules by subgroup D and B members

50 2) Interference studies with fiber protein derived peptides

[0075] Peptides of 6-12 amino acids are synthetically synthesised which together form the complete knob domain of a fiber from a subgroup D, for example 49. Next, one or more peptides are mixed in various concentrations with the 55 fiber 49 chimaeric adenovirus after which the mixture is added to the cells. Using this approach one or more peptides are identified which block, at a certain concentration, the infection of the fiber 49 chimaeric adenovirus. This peptide or these peptides are subsequently used to investigate whether the infection of other subgroup D members is blocked by addition of the peptide(s) and whether inhibition of infection occurs using the same concentration of peptide. Identical

to the example for subgroup D described above peptides are synthesised using the knob domain of a member of subgroup A, B, C, E, and F. These experiments show not only which adherence molecules are used but also which part of the fiber protein is directly involved in binding to target cells. Naturally these peptides are also used to investigate inter-subgroup variation.

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3) Interference studies with baculovirus produced recombinant knob proteins

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[0076] Of each adenovirus subgroup, the knob region of one member is amplified by PCR. The forward oligonucleotide hybridises to the final repeat of the shaft part of the fiber just upstream of the start of the knob protein. This oligonucleotide contains a restriction site to facilitate cloning, a Histidine (6x) tag for purification after production, and a mutation thereby introducing a Methionine start codon. The reverse oligonucleotide hybridises after the polyA signal and contains a restriction site to facilitate cloning into a baculovirus expression construct. After generation of recombinant baculovirus, insect cells for instance SF9, are infected. 4-6 days after infection cells are cracked by 3 cycles of freeze/thaw. Recombinant knob protein is purified from the supernatant using an antibody specifically recognising the His tag. The recombinant knobs are subsequently used in interference studies to investigate the complexity of adenovirus binding between members of different subgroups as well as members within one subgroup.

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Example 7: identification of adherence molecules involved in adenovirus subgroup B, D, and F binding and internalisation

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[0077] To investigate what adherence molecules are involved in binding and internalisation of adenovirus serotypes from different subgroups in particular subgroups B, D, and F, the following strategies are designed.

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1) Phage display libraries

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[0078] Phage display libraries, containing random 6-12 amino acids peptides are mixed with synthetically synthesised peptides which have identified to block infection of one or more members of either subgroup B, D, and/or F. Mixing of phages with peptide(s) is performed in an ELISA setting in which the peptide(s) are coated to a plastic support. Several rounds of mixing, washing and elution are performed to obtain an enrichment for phages that truly and specifically bind to the peptide(s). Finally the phages retrieved are amplified and plaque purified after which approximately 20 are sequenced to establish the nature of the peptide insert of the phages. From the consensus sequence of all 20 phages, a (degenerate) oligonucleotide is synthesised which together with a polyA hybridising oligonucleotide is used for the amplification of cDNA sequences both from cells which can or cannot (negative control) be infected with a subgroup B, D, and/or F chimaeric adenovirus. Amplified cDNAs are cloned, sequenced and aligned, amongst others, against existing Genbank sequences.

2) cDNA expression library screening

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[0079] cDNA libraries, either commercially available or generated using a CAR-negative cell line which is highly transducible with chimaeric adenoviruses carrying the fiber protein of members of for example subgroup D or subgroup F, are used for expression library screening using either radiolabelled adenovirus or recombinant produced knob proteins as probes. Clones or plaques which bind to the probe are picked, amplified and re-tested for enrichment of probe binding. Finally phages are picked after which the cDNA content is elucidated by sequence analysis. Retrieved cDNAs are cloned, sequenced and aligned, amongst others, against existing Genbank sequences.

3) Peptidase treatment of cells after adenovirus binding

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[0080] Cells which are highly transducible with chimaeric adenoviruses carrying the fiber protein of members of for example subgroup D, are treated with different peptidases after binding of the chimaeric adenovirus. The panel of peptidases suited is first tested on the chimaeric adenovirus only to ensure that capsid proteins of the chimaeric virus is not cleaved. Peptidase treated cells are spun down after which the supernatant is added to 24-well plates precoated with anti-adenovirus hexon and/or penton antibodies. After binding of adenovirus to the precoated plastic support, wells are washed extensively with PBS. Upon washing, the adenovirus is harvested after which either protein gel electrophoresis or Malditoff is used to identify whether parts of a cellular protein is bound to the fiber protein or whether extra protein bands are visible as compared to protein gel electrophoresis or Malditoff of a purified batch of adenovirus only. As a negative control for the above described experiments cells negative for infection with a chimaeric adenovirus carrying a fiber of a member of subgroup D can be used. Alternatively, cells which are highly transducible with chimaeric adenoviruses carrying the fiber protein of members of for example subgroup D, are first treated with peptidases after

which the medium is incubated with adenoviruses bound to a plastic support.

[0081] The above described examples encompasses the construction of recombinant adenoviral vectors chimaeric for the fiber protein which results in an altered infection host range. The alteration of the infection host range results in highly efficient infection of cells negative for the CAR protein which is the protein required by adenovirus serotype 5 for efficient infection. These vectors are generated for the purpose of gene transfer and recombinant DNA vaccines. These vectors are thus ideally suited for gene transfer to tissues, and/or organs of which the cells do not express detectable levels of CAR.

Figure and table legends

10 Table 1: Association of human adenovirus serotypes with human disease.

Table 2: Oligonucleotides and degenerate oligonucleotides used for the amplification of DNA encoding for fiber protein derived from alternative human adenovirus serotypes. Bold letters in oligonucleotides A-E represent an NdeI restriction site. Bold letters in oligonucleotides 1-6 and 8 represent an NsiI restriction site. Bold letters in oligonucleotide 7 represents a Pael restriction site.

15 Table 3: Production results of fiber chimaeric adenoviruses. The number of virus particles per ml were determined using HPLC. The number of infectious units (IU) per millilitre were determined through titration on human 911 cells. For infection experiments, the number of virus particles per millilitre is taken from all chimaeric adenoviruses since IU/ml reflects a receptor mediated process.

20 Table 4: Flow cytometric results on expression of integrins $\alpha_v\beta_3$ and $\alpha_v\beta_5$, the Coxsackie adenovirus receptor (CAR), and MHC class I on the membranes of human cell lines and human primary cells. A549: Human lung carcinoma cell line (ATCC, CCL-1185). K562: Human erythroid leukemia (ATCC, CCL-243). SupT1: Human Lymphoblast hybrid B and T (ATCC, CRL-1991). GM09503: Human primary fibroblasts. HEPG2: Human liver carcinoma (ATCC, HB8065). CEM: human lymphoblast cells (ATCC, CRL-1992). HeLa: Human cervix carcinoma (ATCC, CCL-2). Primary amniocytes and chorion villi cells were obtained from department of antropogenetics, Leiden, The Netherlands. Primary Smooth muscle cells, Human umbilical vein endothelial cells, and synoviocytes were obtained from TNO-PG, Leiden, The Netherlands. Shown is the percentage of cells expressing either molecule on their membrane. ND: not determined. 0% means undetectable expression of the molecule on the membrane of the cell using flow cytometry. 100% means high expression of the molecule on the cell membrane.

[0082] Figure 1: Schematic presentation of adapter plasmid pMLP1.TK.

[0083] Figure 2: Schematic presentation of adapter plasmid pAd/L420-HAS.

35 [0084] Figure 3: Schematic presentation of adapter plasmid pAd5/CLIP

[0085] Figure 4: Schematic presentation of plasmid system which requires only one recombinational event to generate recombinant adenoviruses.

[0086] Figure 5: Schematic presentation of plasmid system which requires two recombinational events to generate recombinant adenoviruses.

40 [0087] Figure 6: Schematic presentation of generation of plasmid pBr/AdBamRDeltaFib in which the Adenovirus type 5 fiber DNA is replaced by a short DNA stretch containing an unique NsiI site.

[0088] Figure 7: Fiber protein sequences of adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 42, 43, 44, 45, 46, 47, 48, 49, and 51. Bold letters represent part of the tail of adenovirus serotype 5. If bold letters not present it means that a PCR fragment was sequenced which does not contain the Ad5 tail. An X, present in the sequence means unidentified amino acid due to unidentified nucleotide. At the end of the sequence the stop codon of the fiber is presented by a dot.

[0089] Figure 8: Transduction of human lung carcinoma cells (A549) with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 17, 28, 32, 40-L, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500 (see legend on the right of graph). Luciferase transgene expression is expressed as relative light units (RLU) per μ g of protein.

50 [0090] Figure 9: Transduction of human erythroid leukemia cells (K562) with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 28, 32, 40-S, 40-L, 49, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500, 5000 (see legend on the right of graph). Luciferase transgene expression is expressed as relative light units (RLU) per μ g of protein. Error bars represent SD.

[0091] Figure 10: Transduction of human primary fibroblasts (GM09503) with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 28, 32, 40-L, 49, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500, 5000 (see legend on the right of graph).

Luciferase transgene expression is expressed as relative light units (RLU) per µg of protein. Error bars represent SD.

[0092] Figure 11: Transduction of human lymphoblast cells (SupT1) with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 28, 32, 40-S, 40-L, 49, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500, 5000 (see legend on the right of graph).

5 Luciferase transgene expression is expressed as relative light units (RLU) per µg of protein. Error bars represent SD.

[0093] Figure 12: Transduction of human chorion villi cells with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 28, 32, 40-L, 49, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500, 5000 (see legend on the right of graph). Luciferase transgene expression is expressed as relative light units (RLU) per µg of protein. Error bars represent SD.

10 [0094] Figure 13: Transduction of human hepatic cells (HEPG2) with a panel of chimaeric adenoviruses carrying the fiber of adenovirus 12, 16, 28, 32, 40-S, 40-L, 49, or 51. Adenovirus 5 served as reference. Cells were infected with increasing MOI based on virus particles per cell: 10, 50, 250, 1250, 2500, 5000 (see legend on the right of graph). Luciferase transgene expression is expressed as relative light units (RLU) per µg of protein. Error bars represent SD.

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Tables and figures

[0137]

45

Table 1

Syndrom	Subgenus	Serotype
Respiratory illness	A	31
	B	3, 7, 11, 14, 21, 34, 35, 51
	C	1,2,5,6
	D	39, 42-48
	E	4
Keratoconjunctivitis (eye)	B	11
	D	8, 19, 37, 50
Hemorrhagic cystitis (Kidney) And urogenital tract infections	B	7, 11, 14, 16, 21, 34, 35
	C	5

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Table 1 (continued)

Syndrom	Subgenus	Serotype
5	D	39, 42-48
Sexual transmission	C	2
	D	19, 37
10	A	31
Gastroenteritis	B	3
	C	1, 2, 5
	D	28
CNS disease	F	40, 41
	A	12, 31
	B	3, 7
15	C	2, 5, 6
Hepatitis	D	32, 49
	A	31
	C	1, 2, 5
20	A	31
Disseminated	B	3, 7, 11, 21
	D	30, 43-47
25	A	18
None (???)	D	9, 10, 13, 15 17, 20, 22-29, 33, 36, 38

Table 2

Serotype	Tail oligonucleotide	Knob oligonucleotide
30	A	1
4		
8	B	2
9	B	2
12	E	3
16	C	4
35		
19p	B	2
28	B	2
32	B	2
36	B	2
40		
37	B	2
40-1	D	5
40-2	D	6
41-s	D	5
41-1	D	7
45		
49	B	2
50		
A: 5'- CCC GTG TAT CCA TAT GAT GCA GAC AAC GAC CGA CC- 3'		
B: 5'- CCC GTC TAC CCA TAT GGC TAC GCG CGG- 3'		
C: 5'- CCK GTS TAC CCA TAT GAA GAT GAA AGC- 3'		
D: 5'- CCC GTC TAC CCA TAT GAC ACC TYC TCA ACT C- 3'		
E: 5'- CCC GTT TAC CCA TAT GAC CCA TTT GAC ACA TCA GAC- 3'		
1: 5"- CCG ATG CAT TTA TTG TTG GGC TAT ATA GGA - 3'		
2: 5'- CCG ATG CAT TYA TTC TTG GGC RAT ATA GGA - 3'		
3: 5'- CCG ATG CAT TTA TTC TTG GGR AAT GTA WGA AAA GGA - 3'		
4: 5'- CCG ATG CAT TCA GTC ATC TTC TCT GAT ATA - 3'		

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Table 2 (continued)

Serotype	Tail oligonucleotide	Knob oligonucleotide
50	B	2
51	C	8
5: 5'- CCG ATG CAT TTA TTG TTC AGT TAT GTA GCA - 3'		
6: 5'- GCC ATG CAT TTA TTG TTC TGT TAC ATA AGA - 3'		
7: 5' - CCG TTA ATT AAG CCC TTA TTG TTC TGT TAC ATA AGA A - 3'		
8: 5'- CCG ATG CAT TCA GTC ATC YTC TWT AAT ATA - 3'		

5

10

Table 3

Adenovirus	Virus particles/ ml	Infectious units/ ml
Ad5Fib5	2.2 x 10 ¹²	6.8 x 10 ¹¹
Ad5Fib12	4.4 x 10 ¹²	1.9 x 10 ¹²
Ad5Fib16	1.4 x 10 ¹²	3.0 x 10 ¹⁰
Ad5Fib17	9.3 x 10 ¹¹	9.5 x 10 ⁹
Ad5Fib28	5.4 x 10 ¹⁰	2.8 x 10 ⁸
Ad5Fib32	2.0 x 10 ¹²	1.1 x 10 ¹²
Ad5Fib40-S	3.2 x 10 ¹⁰	1.0 x 10 ¹⁰
Ad5Fib40-L	2.0 x 10 ¹²	6.4 x 10 ¹¹
Ad5Fib49	1.2 x 10 ¹²	4.3 x 10 ¹¹
Ad5Fib51	5.1 x 10 ¹²	1.0 x 10 ¹²

15

20

25

30

Table 4

Cell line	$\alpha_v\beta 3$	$\alpha_v\beta 5$	CAR	MHC class I
A549	17%	98%	100%	ND
K562	12%	55%	0%	15%
GM09503	20%	50%	0%	100%
CEM	0%	0%	3%	100%
SupT1	5%	1%	70%	100%
Smooth muscle cells	100%	70%	0%	15%
HUVEC	100%	15%	10%	90%
Synoviocytes	30%	40%	0%	100%
1 ⁰ chorionvilli	100%	0%	12%	100%
HepG2	0%	10%	100%	80%

35

40

45

50

55

Annex to the application documents - subsequently filed sequences listing

[0138]

5

SEQUENCE LISTING

<110> Introgen BV

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for the adenovirus serotype 5 Coxsacki adenovirus
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			160
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	240		
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	Pro Thr Ser Asn Leu Ser Lys Glu Tyr Trp Asn Tyr Arg Ser Tyr Asp		
	275	280	285
15	Asn Asn Ile Gly Thr Pro Tyr Glu Asn Ala Val Pro Phe Met Pro Asn		
	290	295	300
	Leu Lys Ala Tyr Pro Lys Pro Thr Lys Thr Ala Ser Asp Lys Ala Glu		
	305	310	315
	320		
20	Asn Lys Ile Ser Ser Ala Lys Asn Lys Ile Val Ser Asn Phe Tyr Phe		
	325	330	335
	Gly Gly Gln Ala Tyr Gln Pro Gly Thr Ile Ile Ile Lys Phe Asn Glu		
	340	345	350
25	Glu Ile Asp Glu Thr Cys Ala Tyr Ser Ile Thr Phe Asn Phe Gly Trp		
	355	360	365
	Gly Lys Val Tyr Asp Asn Pro Phe Pro Asp Thr Thr Ser Phe Thr		
	370	375	380
30	Xaa Ser Tyr Ile Ala Gln Glu		
	385	390	
35	<210> 33		
	<211> 290		
	<212> PRT		
	<213> adenoviridae		
40	<220>		
	<221> VARIANT		
	<222> (1)...(290)		
	<223> /note="Serotype 14 fiber protein"		
	<400> 33		
45	His Pro Phe Ile Asn Pro Gly Phe Ile Ser Pro Asn Gly Phe Thr Gln		
	1	5	10
	15		
	Ser Pro Asp Gly Val Leu Thr Leu Lys Cys Leu Thr Pro Leu Thr Thr		
	20	25	30
50	Thr Gly Gly Ser Leu Gln Leu Lys Val Gly Gly Leu Thr Val Asp		
	35	40	45
	Asp Thr Asp Gly Thr Leu Gln Glu Asn Ile Gly Ala Thr Thr Pro Leu		
	50	55	60
55	Val Lys Thr Gly His Ser Ile Gly Leu Ser Leu Gly Ala Gly Leu Gly		

	65	70	75	80
5	Thr Asp Glu Asn Lys Leu Cys Thr Lys Leu Gly Glu Gly Leu Thr Phe 85		90	95
10	Asn Ser Asn Asn Ile Cys Ile Asp Asp Asn Ile Asn Thr Leu Trp Thr 100	105		110
15	Gly Val Asn Pro Thr Glu Ala Asn Cys Gln Met Met Asp Ser Ser Glu 115	120	125	
20	Ser Asn Asp Cys Lys Leu Ile Leu Thr Leu Val Lys Thr Gly Ala Leu 130	135	140	
25	Val Thr Ala Phe Val Tyr Val Ile Gly Val Ser Asn Asn Phe Asn Met 145	150	155	160
30	Leu Thr Thr Tyr Arg Asn Ile Asn Phe Thr Ala Glu Leu Phe Phe Asp 165	170		175
35	Ser Ala Gly Asn Leu Leu Thr Ser Leu Ser Ser Leu Lys Thr Pro Leu 180	185	190	
40	Asn His Lys Ser Gly Gln Thr Trp Leu Leu Val Pro Leu Leu Met Leu 195	200	205	
45	Lys Val Ser Cys Pro Ala Gln Leu Leu Ile Leu Ser Ile Ile Ile Leu 210	215	220	
50	Glu Lys Asn Lys Thr Thr Phe Thr Glu Leu Val Thr Thr Gln Leu Val 225	230	235	240
55	Ile Thr Leu Leu Phe Pro Leu Thr Ile Ser Val Met Leu Asn Gln Arg 245	250	255	
	Ala Ile Arg Ala Asp Thr Ser Tyr Cys Ile Arg Ile Thr Trp Ser Trp 260	265	270	
	Asn Thr Gly Asp Ala Pro Glu Gly Gln Thr Ser Ala Thr Thr Leu Val 275	280	285	
	Thr Ser 290			
	<210> 34			
	<211> 345			
	<212> PRT			
	<213> adenoviridae			
	<220>			
	<221> VARIANT			
	<222> (1)..(345)			
	<223> /note="Serotype 20 fiber protein"			
	<400> 34			
	Ile Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly 1	5	10	15
	Leu Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro			

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	20	25	30
	Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly Gly Ile		
5	35	40	45
	Thr Val Glu Gln Asp Ser Gly Gln Leu Ile Ala Asn Pro Lys Ala Pro		
	50	55	60
10	Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr Ala Tyr Pro Phe		
	65	70	75
	Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly Gln Gly Leu Lys		
	85	90	95
15	Val Leu Asp Glu Lys Asp Ser Gly Gly Leu Gln Asn Leu Leu Gly Lys		
	100	105	110
	Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu Glu Leu Lys Asn		
	115	120	125
20	Pro Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val Arg Leu Gly Lys		
	130	135	140
	Asp Gly Gly Leu Ser Phe Asn Lys Asn Gly Glu Leu Val Ala Trp Asn		
	145	150	155
	160		
25	Lys His Asn Asp Thr Gly Thr Leu Trp Thr Pro Asp Pro Ser Pro		
	165	170	175
	Asn Cys Lys Ile Glu Glu Val Lys Asp Ser Lys Leu Thr Leu Val Leu		
	180	185	190
30	Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Met Ala Phe Gln Val Val		
	195	200	205
	Lys Gly Thr Tyr Glu Asn Ile Ser Lys Asn Thr Ala Lys Asn Ser Phe		
	210	215	220
35	Ser Ile Lys Leu Leu Phe Asp Asp Asn Gly Lys Leu Leu Glu Gly Ser		
	225	230	235
	240		
	Ser Leu Asp Lys Asp Tyr Trp Asn Phe Arg Ser Asp Asp Ser Ile Ile		
	245	250	255
40	Pro Asn Gln Tyr Asp Asn Ala Val Pro Phe Met Pro Asn Leu Lys Ala		
	260	265	270
	Tyr Pro Lys Pro Ser Thr Val Leu Pro Ser Thr Asp Lys Asn Ser Asn		
	275	280	285
45	Gly Lys Asn Thr Ile Val Ser Asn Leu Tyr Leu Glu Gly Lys Ala Tyr		
	290	295	300
	Gln Pro Val Ala Val Thr Ile Thr Phe Asn Lys Glu Ile Gly Cys Thr		
	305	310	315
	320		
50	Tyr Ser Ile Thr Phe Asp Phe Gly Trp Ala Lys Thr Tyr Asp Val Pro		
	325	330	335
	Ile Pro Phe Asp Ser Ser Ser Phe Thr		
55	340	345	

5 <210> 35
 <211> 346
 <212> PRT
 <213> adenoviridae

 10 <220>
 <221> VARIANT
 <222> (1)..(346)
 <223> /note="Serotype 23 fiber protein"

 15 <400> 35
 Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe
 1 5 10 15

 Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile
 20 25 30

 20 Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Gly Leu Thr
 35 40 45

 Val Glu Gln Asp Ser Gly Asn Leu Lys Val Asn Thr Lys Ala Pro Leu
 50 55 60

 25 Gln Val Ala Ala Asp Lys Gln Leu Glu Ile Ala Leu Ala Asp Pro Phe
 65 70 75 80

 Glu Val Ser Lys Gly Arg Leu Gly Ile Lys Ala Gly His Gly Leu Lys
 85 90 95

 30 Val Ile Asp Asn Ser Ile Ser Gly Leu Glu Gly Leu Val Gly Thr Leu
 100 105 110

 Val Val Leu Thr Gly His Gly Ile Gly Thr Glu Asn Leu Leu Asn Asn
 115 120 125

 35 Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg Leu Gly Lys Asp
 130 135 140

 Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Leu Val Ala Trp Asn Lys
 145 150 155 160

 40 Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn
 165 170 175

 Cys Lys Val Ile Glu Ala Lys Asp Ser Lys Leu Thr Leu Val Leu Thr
 180 185 190

 45 Lys Cys Gly Ser Gln Ile Leu Ala Asn Met Ser Leu Leu Ile Leu Lys
 195 200 205

 Gly Thr Tyr Glu Tyr Ile Ser Asn Ala Ile Ala Asn Lys Ser Phe Thr
 210 215 220

 50 Ile Lys Leu Leu Phe Asn Asp Lys Gly Val Leu Met Asp Gly Ser Ser
 225 230 235 240

 Leu Asp Lys Asp Tyr Trp Asn Tyr Lys Ser Asp Asp Ser Val Met Ser
 245 250 255

Lys Ala Tyr Glu Asn Ala Val Pro Phe Met Pro Asn Leu Lys Ala Tyr
 260 265 270
 5 Pro Asn Pro Thr Thr Ser Thr Thr Asn Pro Ser Thr Asp Lys Lys Ser
 275 280 285
 Asn Gly Lys Asn Ala Ile Val Ser Asn Val Tyr Leu Glu Gly Arg Ala
 290 295 300
 10 Tyr Gln Pro Val Ala Ile Thr Ile Thr Phe Asn Lys Glu Thr Gly Cys
 305 310 315 320
 Thr Tyr Ser Met Thr Phe Asp Phe Gly Trp Ser Lys Val Tyr Asn Asp
 325 330 335
 15 Pro Ile Pro Phe Asp Thr Ser Ser Leu Thr
 340 345
 20 <210> 36
 <211> 390
 <212> PRT
 <213> adenoviridae
 25 <220>
 <221> VARIANT
 <222> (1)...(390)
 <223> /note="Serotype 24 fiber protein"
 30 <400> 36
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15
 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30
 35 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45
 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60
 40 Leu Ala Asp Pro Ile Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val
 65 70 75 80
 Gly Gly Gly Leu Thr Val Glu Lys Asp Ser Gly Asn Leu Lys Val Asn
 85 90 95
 45 Pro Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Gln Leu Glu Ile Ala
 100 105 110
 Leu Ala Tyr Pro Phe Glu Val Ser Asn Gly Lys Leu Gly Ile Lys Ala
 115 120 125
 50 Gly His Gly Leu Lys Val Ile Asp Lys Ile Ala Gly Leu Glu Gly Leu
 130 135 140
 Ala Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Asn
 145 150 155 160
 55

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	Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr			
	20	25	30	
5	Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val			
	35	40	45	
	Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys			
	50	55	60	
10	Leu Ala Asp Pro Ile Thr Ile Ser Asn Gly Asp Val Ser Leu Lys Val			
	65	70	75	80
	Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Asn Leu Ser Val Asn			
	85	90	95	
15	Pro Lys Ala Pro Leu Gln Val Gly Thr Asp Lys Lys Leu Glu Leu Ala			
	100	105	110	
	Leu Ala Pro Pro Phe Asn Val Lys Asp Asn Lys Leu Asp Leu Leu Val			
	115	120	125	
20	Gly Asp Gly Leu Lys Val Ile Asp Lys Ser Ile Ser Xaa Leu Pro Gly			
	130	135	140	
	Leu Leu Asn Tyr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Asn Glu			
	145	150	155	160
25	Glu Leu Lys Asn Asp Asp Gly Ser Asn Lys Gly Val Gly Leu Cys Val			
	165	170	175	
	Arg Ile Gly Glu Gly Gly Leu Thr Phe Asp Asp Lys Gly Tyr Leu			
30	180	185	190	
	Val Ala Trp Asn Lys Lys His Asp Ile Arg Thr Leu Trp Thr Thr Leu			
	195	200	205	
	Asp Pro Ser Pro Asn Cys Arg Ile Asp Val Asp Lys Asp Ser Lys Leu			
35	210	215	220	
	Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser			
	225	230	235	240
40	Leu Leu Val Val Lys Gly Arg Phe Gln Asn Leu Asn Tyr Lys Thr Asn			
	245	250	255	
	Pro Asn Leu Pro Lys Thr Phe Thr Ile Lys Leu Leu Phe Asp Glu Asn			
	260	265	270	
45	Gly Ile Leu Lys Asp Ser Ser Asn Leu Asp Lys Asn Tyr Trp Asn Tyr			
	275	280	285	
	Arg Asn Gly Asn Ser Ile Leu Ala Glu Gln Tyr Lys Asn Ala Val Gly			
	290	295	300	
50	Phe Met Pro Asn Leu Ala Ala Tyr Pro Lys Ser Thr Thr Thr Gln Ser			
	305	310	315	320
	Lys Leu Tyr Ala Arg Asn Thr Ile Phe Gly Asn Ile Tyr Leu Asp Ser			
	325	330	335	

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Gln Ala Tyr Asn Pro Val Val Ile Lys Ile Thr Phe Asn Gln Glu Ala
 340 345 350

5 Asp Ser Ala Tyr Ser Ile Thr Leu Asn Tyr Ser Trp Gly Lys Asp Tyr
 355 360 365

Glu Asn Ile Pro Phe Asp Ser
 370 375

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<210> 38
 <211> 335
 <212> PRT
 <213> adenoviridae

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<220>
 <221> VARIANT
 <222> (1)..(335)
 <223> /note="Serotype 27 fiber protein"

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<400> 38
 Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn
 1 5 10 15

25

Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile
 20 25 30

Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Leu Val Val Glu
 35 40 45

30

Lys Glu Ser Gly Lys Leu Ser Val Asp Pro Lys Thr Pro Leu Gln Val
 50 55 60

Ala Ser Asp Asn Lys Leu Glu Leu Ser Tyr Asn Ala Pro Phe Lys Val
 65 70 75 80

35

Glu Asn Asp Lys Leu Ser Leu Asp Val Gly His Gly Leu Lys Val Ile
 85 90 95

Gly Asn Glu Val Ser Ser Leu Pro Gly Leu Ile Asn Lys Leu Val Val
 100 105 110

40

Leu Thr Gly Lys Gly Ile Gly Thr Glu Glu Leu Lys Glu Gln Asn Ser
 115 120 125

Asp Lys Ile Ile Gly Val Gly Ile Asn Val Arg Ala Arg Gly Gly Leu
 130 135 140

45

Ser Phe Asp Asn Asp Gly Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp
 145 150 155 160

Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Met
 165 170 175

50

Leu Thr Lys Lys Asp Ser Lys Leu Thr Leu Thr Lys Cys Gly
 180 185 190

Ser Gln Ile Leu Gly Asn Val Ser Leu Leu Ala Val Ser Gly Lys Tyr
 195 200 205

55

Leu Asn Met Thr Lys Asp Glu Thr Gly Val Lys Ile Ile Leu Leu Phe
 210 215 220

5 Asp Arg Asn Gly Val Leu Met Gln Glu Ser Ser Leu Asp Lys Glu Tyr
 225 230 235 240

Trp Asn Tyr Arg Asn Asp Asn Asn Val Ile Gly Thr Pro Tyr Glu Asn
 245 250 255

10 Ala Val Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Thr Ser
 260 265 270

Ala Asp Ala Lys Asn Tyr Ser Arg Ser Lys Ile Ile Ser Asn Val Tyr
 275 280 285

15 Leu Lys Gly Leu Ile Tyr Gln Pro Val Ile Ile Ala Ser Phe Asn
 290 295 300

Gln Glu Thr Thr Asn Gly Cys Val Tyr Ser Ile Ser Phe Asp Phe Thr
 305 310 315 320

20 Cys Ser Lys Asp Tyr Thr Gly Gln Gln Phe Asp Val Thr Ser Phe
 325 330 335

25 <210> 39
 <211> 374
 <212> PRT
 <213> adenoviridae

30 <220>
 <221> VARIANT
 <222> (1)..(374)
 <223> /note="Serotype 28 fiber protein"

35 <400> 39
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15

Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30

40 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45

Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60

45 Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asp Val Ser Leu Lys Leu
 65 70 75 80

Gly Gly Gly Leu Thr Val Glu Lys Glu Ser Gly Asn Leu Thr Val Asn
 85 90 95

50 Pro Lys Ala Pro Leu Gln Val Ala Ser Gly Gln Leu Glu Leu Ala Tyr
 100 105 110

55 Tyr Ser Pro Phe Asp Val Lys Asn Asn Met Leu Thr Leu Lys Ala Gly
 115 120 125

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His Gly Leu Ala Val Val Thr Lys Asp Asn Thr Asp Leu Gln Pro Leu
 130 135 140

5 Met Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Gly Thr
 145 150 155 160

Ser Ala His Gly Gly Thr Ile Asp Val Arg Ile Gly Lys Asn Gly Ser
 165 170 175

10 Leu Ala Phe Asp Lys Asn Gly Asp Leu Val Ala Trp Asp Lys Glu Asn
 180 185 190

Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys
 195 200 205

15 Met Ser Glu Val Lys Asp Ser Lys Leu Thr Leu Ile Leu Thr Lys Cys
 210 215 220

Gly Ser Gln Ile Leu Gly Ser Val Ser Leu Leu Ala Val Lys Gly Glu
 225 230 235 240

20 Tyr Gln Asn Met Thr Ala Ser Thr Asn Lys Asn Val Lys Ile Thr Leu
 245 250 255

Leu Phe Asp Ala Asn Gly Val Leu Leu Glu Gly Ser Ser Leu Asp Lys
 260 265 270

25 Glu Tyr Trp Asn Phe Arg Asn Asn Asp Ser Thr Val Ser Gly Lys Tyr
 275 280 285

Glu Asn Ala Val Pro Phe Met Pro Asn Ile Thr Ala Tyr Lys Pro Val
 290 295 300

30 Asn Ser Lys Ser Tyr Ala Arg Ser His Ile Phe Gly Asn Val Tyr Ile
 305 310 315 320

Asp Ala Lys Pro Tyr Asn Pro Val Val Ile Lys Ile Ser Phe Asn Gln
 325 330 335

Glu Thr Gln Asn Asn Cys Val Tyr Ser Ile Ser Phe Asp Tyr Thr Cys
 340 345 350

35 Ser Lys Glu Tyr Thr Gly Met Gln Phe Asp Val Thr Ser Phe Thr Phe
 355 360 365

Ser Tyr Ile Ala Gln Glu
 370

40

<210> 40
 <211> 343
 <212> PRT
 50 <213> adenoviridae

<220>
 <221> VARIANT
 <222> (1)..(343)
 <223> /note="Serotype 29 fiber protein"

55 <400> 40

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Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe
 1 5 10 15

Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile
 5 20 25 30

Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Gly Leu Thr
 35 40 45

Val Glu Gln Asp Ser Gly Asn Leu Ser Val Asn Pro Lys Ala Pro Leu
 10 50 55 60

Gln Val Gly Thr Asp Lys Lys Leu Glu Leu Ala Leu Ala Pro Pro Phe
 65 70 75 80

Asp Val Arg Asp Asn Lys Leu Ala Ile Leu Val Gly Asp Gly Leu Lys
 15 85 90 95

Val Ile Asp Arg Ser Ile Ser Asp Leu Pro Gly Leu Leu Asn Tyr Leu
 100 105 110

Val Val Leu Thr Gly Lys Gly Ile Gly Asn Glu Glu Leu Lys Asn Asp
 20 115 120 125

Asp Gly Ser Asn Lys Gly Val Gly Leu Cys Val Arg Ile Gly Glu Gly
 25 130 135 140

Gly Gly Leu Thr Phe Asp Asp Lys Gly Tyr Leu Val Ala Trp Asn Asn
 145 150 155 160

Lys His Asp Ile Arg Thr Leu Trp Thr Thr Leu Asp Pro Ser Pro Asn
 30 165 170 175

Cys Lys Ile Asp Ile Glu Lys Asp Ser Lys Leu Thr Leu Val Leu Thr
 180 185 190

Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Ile Val Asn
 35 195 200 205

Gly Lys Phe Lys Ile Leu Asn Asn Lys Thr Asp Pro Ser Leu Pro Lys
 210 215 220

Ser Phe Asn Ile Lys Leu Leu Phe Asp Gln Asn Gly Val Leu Leu Glu
 40 225 230 235 240

Asn Ser Asn Ile Glu Lys Gln Tyr Leu Asn Phe Arg Ser Gly Asp Ser
 245 250 255

Ile Leu Pro Glu Pro Tyr Lys Asn Ala Ile Gly Phe Met Pro Asn Leu
 45 260 265 270

Leu Ala Tyr Ala Lys Ala Thr Thr Asp Gln Ser Lys Ile Tyr Ala Arg
 275 280 285

Asn Thr Ile Tyr Gly Asn Ile Tyr Leu Asp Asn Gln Pro Tyr Asn Pro
 50 290 295 300

Val Val Ile Lys Ile Thr Phe Asn Asn Glu Ala Asp Ser Ala Tyr Ser
 55 305 310 315 320

Ile Thr Phe Asn Tyr Ser Trp Thr Lys Asp Tyr Asp Asn Ile Pro Phe

325

330

335

Asp Ser Thr Ser Phe Thr Ser
 5 340

10 <210> 41
 <211> 386
 <212> PRT
 <213> adenoviridae

15 <220>
 <221> VARIANT
 <222> (1)..(386)
 <223> /note="Serotype 30 fiber protein"

20 <400> 41
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15

25 Lys Arg Ala Arg Pro Ser Xaa Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30

30 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Xaa Thr Pro Pro Phe Val
 35 40 45

35 Xaa Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60

40 Leu Ala Asp Pro Ile Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val
 65 70 75 80

45 Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Asn Leu Ser Val Asn
 85 90 95

50 Xaa Lys Ala Pro Leu Gln Val Gly Thr Asp Lys Lys Leu Glu Leu Ala
 100 105 110

55 Leu Ala Pro Pro Phe Asp Val Arg Asp Asn Lys Leu Ala Ile Leu Val
 115 120 125

60 Gly Asp Gly Leu Lys Val Ile Asp Arg Ser Ile Ser Asp Leu Pro Gly
 130 135 140

65 Leu Leu Asn Tyr Leu Val Val Xaa Thr Gly Lys Gly Ile Gly Asn Glu
 145 150 155 160

70 Glu Leu Lys Asn Asp Asp Gly Ser Asn Lys Gly Val Gly Leu Cys Val
 165 170 175

75 Arg Ile Gly Glu Gly Gly Leu Thr Xaa Asp Asp Lys Gly Tyr Leu
 180 185 190

80 Val Ala Trp Asn Asn Lys His Asp Ile Arg Thr Leu Trp Thr Thr Leu
 195 200 205

85 Asp Pro Ser Pro Asn Cys Lys Ile Asp Ile Glu Lys Asp Ser Lys Leu
 210 215 220

90 Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser

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	225	230	235	240
	Leu Ile Ile Val Asn Gly Lys Phe Lys Ile Leu Asn Asn Lys Thr Asp			
5	245	250	255	
	Pro Ser Leu Pro Lys Ser Phe Asn Ile Lys Leu Leu Phe Asp Gln Asn			
	260	265	270	
10	Gly Val Leu Leu Glu Asn Ser Asn Ile Glu Lys Gln Tyr Leu Asn Phe			
	275	280	285	
	Arg Ser Gly Asp Ser Ile Leu Pro Glu Pro Tyr Lys Asn Ala Ile Gly			
	290	295	300	
15	Phe Met Pro Asn Leu Leu Ala Tyr Ala Lys Ala Thr Thr Asp Gln Ser			
	305	310	315	320
	Lys Ile Tyr Ala Arg Asn Thr Ile Tyr Gly Asn Ile Tyr Leu Asp Asn			
	325	330	335	
20	Gln Pro Tyr Asn Pro Val Val Ile Lys Ile Thr Phe Asn Asn Glu Ala			
	340	345	350	
	Asp Ser Ala Tyr Ser Ile Thr Phe Asn Tyr Ser Trp Thr Lys Asp Tyr			
	355	360	365	
25	Asp Asn Ile Pro Phe Asp Ser Thr Ser Phe Thr Phe Ser Tyr Ile Ala			
	370	375	380	
	Gln Glu			
	385			
30				
	<210> 42			
	<211> 391			
	<212> PRT			
35	<213> adenoviridae			
	<220>			
	<221> VARIANT			
	<222> (1)..(391)			
40	<223> /note="Serotype 32 fiber protein"			
	<400> 42			
	Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met			
	1	5	10	15
45	Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr			
	20	25	30	
	Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val			
	35	40	45	
50	Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys			
	50	55	60	
	Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asn Val Ser Leu Lys Val			
	65	70	75	80
55	Gly Gly Gly Leu Thr Leu Glu Gln Asp Ser Gly Lys Leu Ile Val Asn			

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	85	90	95
5	Pro Lys Ala Pro Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr 100	105	110
	Ala Asp Pro Phe Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly 115	120	125
10	His Gly Leu Lys Val Leu Asp Glu Lys Asn Ala Gly Gly Leu Lys Asp 130	135	140
	Leu Ile Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu 145	150	155
15	Glu Leu Lys Asn Ala Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val 165	170	175
	Arg Leu Gly Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Leu 180	185	190
20	Val Ala Trp Asn Lys His Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro 195	200	205
	Asp Pro Ser Pro Asn Cys Thr Ile Asp Glu Glu Arg Asp Ser Lys Leu 210	215	220
25	Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser 225	230	235
	Leu Leu Val Val Lys Gly Lys Phe Ser Asn Ile Asn Asn Asn Thr Asn 245	250	255
30	Pro Thr Asp Lys Lys Ile Thr Val Lys Leu Leu Phe Asn Glu Lys Gly 260	265	270
	Val Leu Met Asp Ser Ser Leu Lys Lys Glu Tyr Trp Asn Tyr Arg 275	280	285
35	Asn Asp Asn Ser Thr Val Ser Gln Ala Tyr Asp Asn Ala Val Pro Phe 290	295	300
	Met Pro Asn Ile Lys Ala Tyr Pro Lys Pro Thr Thr Asp Thr Ser Ala 305	310	315
40	Lys Pro Glu Asp Lys Lys Ser Ala Ala Lys Arg Tyr Ile Val Ser Asn 325	330	335
	Val Tyr Ile Gly Gly Leu Pro Asp Lys Thr Val Val Ile Thr Ile Lys 340	345	350
45	Leu Asn Ala Glu Thr Glu Ser Ala Tyr Ser Met Thr Phe Glu Phe Thr 355	360	365
50	Trp Ala Lys Thr Phe Glu Asn Leu Gln Phe Asp Ser Ser Ser Phe Thr 370	375	380
	Phe Ser Tyr Ile Ala Gln Glu 385	390	

<210> 43
 <211> 390
 <212> PRT
 <213> adenoviridae
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 <220>
 <221> VARIANT
 <222> (1)..(390)
 <223> /note="Serotype 33 fiber protein"
 10
 <400> 43
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15
 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 15 20 25 30
 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45
 20 Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60
 Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys Val
 65 70 75 80
 25 Gly Gly Gly Leu Thr Leu Gln Glu Gly Ser Leu Thr Val Asn Pro Lys
 85 90 95
 Ala Pro Leu Gln Leu Ala Asn Asp Lys Lys Leu Glu Leu Val Tyr Asp
 100 105 110
 30 Asp Pro Phe Glu Val Ser Thr Asn Lys Leu Ser Leu Lys Val Gly His
 115 120 125
 Gly Leu Lys Val Leu Asp Asp Lys Ser Ala Gly Gly Leu Gln Asp Leu
 130 135 140
 35 Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Ile Glu Asn
 145 150 155 160
 Leu Gln Asn Asp Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg
 40 165 170 175
 Leu Gly Thr Asp Gly Gly Leu Ser Phe Asp Arg Lys Gly Glu Leu Val
 180 185 190
 45 Ala Trp Asn Arg Lys Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
 195 200 205
 Pro Ser Pro Asn Cys Lys Ala Glu Thr Glu Lys Asp Ser Lys Leu Thr
 210 215 220
 50 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Ile
 225 230 235 240
 Ile Val Leu Lys Gly Lys Tyr Glu Phe Val Lys Lys Glu Thr Glu Pro
 245 250 255
 55 Lys Ser Phe Asp Val Lys Leu Leu Phe Asp Ser Lys Gly Val Leu Leu
 260 265 270

Pro Thr Ser Asn Leu Ser Lys Glu Tyr Trp Asn Tyr Arg Ser Tyr Asp
 275 280 285
 5 Asn Asn Ile Gly Thr Pro Tyr Glu Asn Ala Val Pro Phe Met Pro Asn
 290 295 300
 Leu Lys Ala Tyr Pro Lys Pro Thr Lys Thr Ala Ser Asp Lys Ala Glu
 305 310 315 320
 10 Asn Lys Ile Ser Ser Ala Lys Asn Lys Ile Val Ser Asn Phe Tyr Phe
 325 330 335
 Gly Gly Gln Ala Tyr Gln Pro Gly Thr Ile Ile Ile Lys Phe Asn Glu
 15 340 345 350
 Glu Ile Asp Glu Thr Cys Ala Tyr Ser Ile Thr Phe Asn Phe Gly Trp
 355 360 365
 20 Gly Lys Val Tyr Asp Asn Pro Phe Pro Phe Asp Thr Thr Ser Phe Thr
 370 375 380
 Phe Ser Tyr Ile Ala Gln Glu
 385 390
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 <210> 44
 <211> 337
 <212> PRT
 <213> adenoviridae
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 <220>
 <221> VARIANT
 <222> (1)..(337)
 <223> /note="Serotype 34 fiber protein"
 35
 <400> 44
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15
 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 40 20 25 30
 Glu Asp Glu Ser Thr Ser Gln His Pro Phe Ile Asn Pro Gly Phe Ile
 35 40 45
 Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Lys
 45 50 55 60
 Cys Leu Thr Pro Leu Thr Thr Gly Ser Leu Gln Leu Lys Val
 65 70 75 80
 Gly Gly Gly Leu Thr Val Asp Asp Thr Asp Gly Thr Leu Gln Lys Asn
 50 85 90 95
 Ile Arg Ala Thr Thr Pro Ile Thr Lys Asn Asn His Ser Val Glu Leu
 100 105 110
 55 Thr Ile Gly Asn Gly Leu Glu Thr Gln His Asn Lys Leu Cys Ala Lys
 115 120 125

Leu Gly Asn Gly Leu Lys Phe Asn Asn Gly Asp Ile Cys Ile Lys Asp
 130 135 140

5 Ser Ile Asn Thr Leu Trp Thr Gly Ile Asn Pro Pro Pro Asn Cys Gln
 145 150 155 160

Ile Val Glu Asn Thr Asn Thr Asn Asp Gly Lys Leu Thr Leu Val Leu
 165 170 175

10 Val Lys Asn Gly Gly Leu Val Asn Gly Tyr Val Ser Leu Val Gly Val
 180 185 190

Ser Asp Thr Val Asn Gln Met Phe Thr Gln Lys Thr Ala Asn Ile Gln
 195 200 205

Leu Arg Leu Tyr Phe Asp Ser Ser Gly Asn Leu Leu Thr Asp Glu Ser
 210 215 220

20 Asp Leu Lys Ile Pro Leu Lys Asn Lys Ser Ser Thr Ala Thr Ser Glu
 225 230 235 240

Thr Val Ala Ser Ser Lys Ala Phe Met Pro Ser Thr Thr Ala Tyr Pro
 245 250 255

25 Phe Asn Thr Thr Arg Asp Ser Glu Asn Tyr Ile His Gly Ile Cys
 260 265 270

Tyr Tyr Met Thr Ser Tyr Asp Arg Ser Leu Phe Pro Leu Asn Ile Ser
 275 280 285

30 Ile Met Leu Asn Ser Arg Met Ile Ser Ser Asn Val Ala Tyr Ala Ile
 290 295 300

Gln Phe Glu Trp Asn Leu Asn Ala Ser Glu Ser Pro Glu Lys Gln His
 305 310 315 320

35 Met Thr Leu Thr Thr Ser Pro Phe Phe Phe Ser Tyr Ile Ile Glu Asp
 325 330 335

Asp Asn

40

<210> 45
 <211> 337
 45 <212> PRT
 <213> adenoviridae

<220>
 <221> VARIANT
 <222> (1)..(337)
 50 <223> /note="Serotype 35 fiber protein"

<400> 45
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15

55 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30

Glu Asp Glu Ser Thr Ser Gln His Pro Phe Ile Asn Pro Gly Phe Ile
 35 40 45

5 Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Lys
 50 55 60

Cys Leu Thr Pro Leu Thr Thr Gly Gly Ser Leu Gln Leu Lys Val
 65 70 75 80

10 Gly Gly Gly Leu Thr Val Asp Asp Thr Asp Gly Thr Leu Gln Glu Asn
 85 90 95

Ile Arg Ala Thr Ala Pro Ile Thr Lys Asn Asn His Ser Val Glu Leu
 15 100 105 110

Ser Ile Gly Asn Gly Leu Glu Thr Gln Asn Asn Lys Leu Cys Ala Lys
 115 120 125

20 Leu Gly Asn Gly Leu Lys Phe Asn Asn Gly Asp Ile Cys Ile Lys Asp
 130 135 140

Ser Ile Asn Thr Leu Trp Thr Gly Ile Asn Pro Pro Pro Asn Cys Gln
 145 150 155 160

25 Ile Val Glu Asn Thr Asn Thr Asp Gly Lys Leu Thr Leu Val Leu
 165 170 175

Val Lys Asn Gly Gly Leu Val Asn Gly Tyr Val Ser Leu Val Gly Val
 180 185 190

30 Ser Asp Thr Val Asn Gln Met Phe Thr Gln Lys Thr Ala Asn Ile Gln
 195 200 205

Leu Arg Leu Tyr Phe Asp Ser Ser Gly Asn Leu Leu Thr Glu Glu Ser
 210 215 220

35 Asp Leu Lys Ile Pro Leu Lys Asn Lys Ser Ser Thr Ala Thr Ser Glu
 225 230 235 240

Thr Val Ala Ser Ser Lys Ala Phe Met Pro Ser Thr Thr Ala Tyr Pro
 245 250 255

40 Phe Asn Thr Thr Arg Asp Ser Glu Asn Tyr Ile His Gly Ile Cys
 260 265 270

Tyr Tyr Met Thr Ser Tyr Asp Arg Ser Leu Phe Pro Leu Asn Ile Ser
 45 275 280 285

Ile Met Leu Asn Ser Arg Met Ile Ser Ser Asn Val Ala Tyr Ala Ile
 290 295 300

Gln Phe Glu Trp Asn Leu Asn Ala Ser Glu Ser Pro Glu Ser Asn Ile
 50 305 310 315 320

Met Thr Leu Thr Thr Ser Pro Phe Phe Ser Tyr Ile Thr Glu Asp
 325 330 335

55 Asp Asn

5 <210> 46
 <211> 392
 <212> PRT
 <213> adenoviridae

10 <220>
 <221> VARIANT
 <222> (1)..(392)
 <223> /note="Serotype 36 fiber protein"

15 <400> 46
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15

Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30

20 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45

Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60

25 Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asp Val Ser Leu Lys Val
 65 70 75 80

Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Lys Leu Lys Val Asn
 85 90 95

30 Pro Lys Ile Pro Leu Gln Val Val Asn Asp Gln Leu Glu Leu Ala Thr
 100 105 110

Asp Lys Pro Phe Lys Ile Glu Asn Asn Lys Leu Ala Leu Asp Val Gly
 115 120 125

35 His Gly Leu Lys Val Ile Asp Lys Thr Ile Ser Asp Leu Gln Gly Leu
 130 135 140

Val Gly Lys Leu Val Val Leu Thr Gly Val Gly Ile Gly Thr Glu Thr
 145 150 155 160

40 Leu Lys Asp Lys Asn Asp Lys Val Ile Gly Ser Ala Val Asn Val Arg
 165 170 175

Leu Gly Lys Asp Gly Gly Leu Asp Phe Asn Lys Lys Gly Asp Leu Val
 45 180 185 190

Ala Trp Asn Arg Tyr Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
 195 200 205

50 Pro Ser Pro Asn Cys Lys Val Ser Glu Ala Lys Asp Ser Lys Leu Thr
 210 215 220

Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Leu
 225 230 235 240

55 Leu Ile Val Lys Gly Lys Tyr Gln Thr Ile Ser Glu Ser Thr Ile Pro
 245 250 255

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Lys Asp Gln Arg Asn Phe Ser Val Lys Leu Met Phe Asp Glu Lys Gly
 260 265 270
 5 Lys Leu Leu Asp Lys Ser Ser Leu Asp Lys Glu Tyr Trp Asn Phe Arg
 275 280 285
 Ser Asn Asp Ser Val Val Gly Thr Ala Tyr Asp Asn Ala Val Pro Phe
 290 295 300
 10 Met Pro Asn Leu Lys Ala Tyr Pro Lys Asn Thr Thr Ser Ser Thr
 305 310 315 320
 Asn Pro Asp Asp Lys Ile Ser Ala Gly Lys Lys Asn Ile Val Ser Asn
 325 330 335
 15 Val Tyr Leu Glu Gly Arg Val Tyr Gln Pro Val Ala Leu Thr Val Lys
 340 345 350
 Phe Asn Ser Glu Asn Asp Cys Ala Tyr Ser Ile Thr Phe Asp Phe Val
 355 360 365
 20 Trp Ser Lys Thr Tyr Glu Ser Pro Val Ala Phe Asp Ser Ser Ser Phe
 370 375 380
 Thr Phe Ser Tyr Ile Ala Gln Glu
 385 390
 25
 <210> 47
 <211> 380
 30 <212> PRT
 <213> adenoviridae
 <220>
 <221> VARIANT
 <222> (1)..(380)
 35 <223> /note="Serotype 37 fiber protein"
 <400> 47
 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
 1 5 10 15
 40 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
 20 25 30
 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45
 45 Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60
 Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys Val
 65 70 75 80
 Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro Lys
 85 90 95
 55 Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr Asp
 100 105 110

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Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly His
 115 120 125

5 Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp Leu
 130 135 140

Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Asn
 145 150 155 160

10 Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val Arg
 165 170 175

Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala Trp
 180 185 190

15 Asn Pro Lys Tyr Asp Leu Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser
 195 200 205

Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val
 210 215 220

20 Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val
 225 230 235 240

Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile
 245 250 255

Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu
 260 265 270

30 Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn
 275 280 285

Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn
 290 295 300

35 Leu Val Ala Val Ser Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp
 305 310 315 320

Ile Val Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Gly
 325 330 335

40 Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile
 340 345 350

Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu
 355 360 365

45 Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 370 375 380

50 <210> 48
 <211> 391
 <212> PRT
 <213> adenoviridae

55 <220>
 <221> VARIANT
 <222> (1)..(391)

<223> /note="Serotype 38 fiber protein"

<400> 48

5	Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met				
	1	5	10	15	
	Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr				
	20	25	30		
10	Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Xaa Thr Pro Pro Phe Val				
	35	40	45		
	Xaa Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys				
	50	55	60		
15	Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asn Val Ser Leu Lys Val				
	65	70	75	80	
	Gly Gly Gly Leu Thr Leu Glu Gln Asp Ser Gly Lys Leu Ile Val Asn				
	85	90	95		
20	Xaa Lys Ala Pro Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr				
	100	105	110		
	Ala Asp Pro Phe Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly				
25	115	120	125		
	His Gly Leu Lys Val Leu Asp Glu Lys Asn Ala Gly Gly Leu Lys Asp				
	130	135	140		
30	Leu Ile Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu				
	145	150	155	160	
	Glu Leu Lys Asn Ala Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val				
	165	170	175		
35	Arg Leu Gly Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Xaa				
	180	185	190		
	Val Ala Trp Asn Lys His Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro				
	195	200	205		
40	Asp Pro Ser Pro Asn Cys Thr Ile Asp Glu Glu Arg Asp Ser Lys Leu				
	210	215	220		
	Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser				
	225	230	235	240	
45	Leu Leu Val Val Lys Gly Lys Phe Ser Asn Ile Asn Asn Asn Thr Asn				
	245	250	255		
	Pro Thr Asp Lys Lys Ile Thr Val Lys Leu Leu Phe Asn Glu Lys Gly				
	260	265	270		
50	Val Leu Met Asp Ser Ser Ser Leu Lys Lys Glu Tyr Trp Asn Tyr Arg				
	275	280	285		
	Asn Asp Asn Ser Thr Val Ser Gln Ala Tyr Asp Asn Ala Val Pro Phe				
55	290	295	300		
	Met Pro Asn Ile Lys Ala Tyr Pro Lys Pro Thr Thr Asp Thr Ser Ala				

305	310	315	320
Lys Pro Glu Asp Lys Lys Ser Ala Ala Lys Arg Tyr Ile Val Ser Asn			
5	325	330	335
Val Tyr Ile Gly Gly Leu Pro Asp Lys Thr Val Val Ile Thr Ile Lys			
	340	345	350
Leu Asn Ala Glu Thr Glu Ser Ala Tyr Ser Met Thr Phe Glu Phe Thr			
10	355	360	365
Trp Ala Lys Thr Phe Glu Asn Leu Gln Phe Asp Ser Ser Ser Phe Thr			
	370	375	380
15	Phe Ser Tyr Ile Ala Gln Glu		
	385	390	
20	<210> 49		
	<211> 338		
	<212> PRT		
	<213> adenoviridae		
25	<220>		
	<221> VARIANT		
	<222> (1)..(338)		
	<223> /note="Serotype 39 fiber protein"		
30	<400> 49		
	Ile Arg Ile Ser Pro Ser Ser Leu Pro Pro Leu Ser Pro Pro Met Asp		
	1	5	10
			15
Ser Lys Thr Ser Pro Leu Gly Cys Tyr His Ser Asn Trp Leu Thr Gln			
	20	25	30
35	Ser Pro Ser Pro Met Gly Met Ser His Ser Arg Trp Glu Gly Gly Ser		
	35	40	45
Pro Trp Gln Glu Gly Thr Gly Asp Leu Lys Val Asn Ala Lys Ser Pro			
	50	55	60
40	Leu Gln Val Ala Thr Asn Lys Gln Leu Glu Ile Ala Leu Ala Lys Pro		
	65	70	75
			80
Phe Glu Glu Lys Asp Gly Lys Leu Ala Leu Lys Ile Gly His Gly Leu			
	85	90	95
45	Ala Val Val Asp Glu Asn His Thr His Leu Gln Ser Leu Ile Gly Thr		
	100	105	110
Leu Val Ile Leu Thr Gly Lys Gly Ile Gly Thr Gly Arg Ala Glu Ser			
	115	120	125
50	Gly Gly Thr Ile Asp Val Arg Leu Gly Ser Gly Gly Leu Ser Phe		
	130	135	140
Asp Lys Asp Gly Asn Leu Val Ala Trp Asn Lys Asp Asp Asp Arg Arg			
55	145	150	155
			160
Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Lys Ile Asp Gln			

	165	170	175
5	Asp Lys Asp Ser Lys Leu Thr Phe Val Leu Thr Lys Cys Gly Ser Gln		
	180	185	190
	Ile Leu Ala Asn Met Ser Leu Leu Val Val Lys Gly Lys Phe Ser Met		
	195	200	205
10	Ile Asn Asn Lys Val Asn Gly Thr Asp Asp Tyr Lys Lys Phe Thr Ile		
	210	215	220
	Lys Leu Leu Phe Asp Glu Lys Gly Val Leu Leu Lys Asp Ser Ser Leu		
	225	230	235
	Asp Lys Glu Tyr Trp Asn Tyr Arg Ser Asn Asn Asn Asn Val Gly Ser		
15	245	250	255
	Ala Tyr Glu Glu Ala Val Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro		
	260	265	270
20	Lys Pro Pro Thr Pro Pro Thr Asn Pro Thr Thr Pro Leu Glu Lys Ser		
	275	280	285
	Gln Ala Lys Asn Lys Tyr Val Ser Asn Val Tyr Leu Gly Gly Gln Ala		
	290	295	300
25	Gly Asn Pro Val Ala Thr Thr Val Ser Phe Asn Lys Glu Thr Gly Cys		
	305	310	315
	Thr Tyr Ser Ile Thr Phe Asp Phe Ala Trp Asn Lys Thr Tyr Glu Asn		
	325	330	335
30	Val Gln Cys		
35	<210> 50 <211> 379 <212> PRT <213> adenoviridae		
40	<220> <221> VARIANT <222> (1)..(379) <223> /note="Serotype 42 fiber protein"		
45	<400> 50 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met 1 5 10 15		
50	Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr 20 25 30		
	Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val 35 40 45		
55	Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys 50 55 60		
	Leu Ala Asn Pro Ile Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val		

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	65	70	75	80
5	Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Ile Asp			
	85	90		95
	Thr Lys Thr Pro Leu Gln Val Ala Asn Asn Lys Leu Glu Leu Ala Phe			
	100	105		110
10	Asp Ala Pro Leu Tyr Glu Lys Asn Gly Lys Leu Ala Leu Lys Thr Gly			
	115	120		125
	His Gly Leu Ala Val Leu Thr Lys Asp Ile Gly Ile Pro Glu Leu Ile			
	130	135	140	
15	Gly Ser Leu Val Ile Leu Thr Gly Lys Gly Ile Gly Thr Gly Thr Val			
	145	150	155	160
	Ala Gly Gly Gly Thr Ile Asp Val Arg Leu Gly Asp Asp Gly Gly Leu			
	165	170		175
20	Ser Phe Asp Lys Lys Gly Asp Leu Val Ala Trp Asn Lys Lys Asn Asp			
	180	185		190
	Arg Arg Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Val			
	195	200	205	
25	Ser Glu Asp Lys Asp Ser Lys Leu Thr Leu Ile Leu Thr Lys Cys Gly			
	210	215	220	
	Ser Gln Ile Leu Ala Ser Phe Ser Leu Leu Val Val Xaa Gly Thr Tyr			
	225	230	235	240
30	Thr Thr Val Asp Lys Asn Thr Thr Asn Lys Gln Phe Ser Ile Lys Leu			
	245	250		255
	Leu Phe Asp Ala Asn Gly Lys Leu Lys Ser Glu Ser Asn Leu Ser Gly			
35	260	265		270
	Tyr Trp Asn Tyr Arg Ser Asp Asn Ser Val Val Ser Thr Pro Tyr Asp			
	275	280	285	
40	Asn Ala Val Pro Phe Met Pro Asn Thr Thr Ala Tyr Pro Lys Ile Ile			
	290	295	300	
	Asn Ser Thr Thr Asp Pro Glu Asn Lys Lys Ser Ser Ala Lys Lys Thr			
	305	310	315	320
45	Ile Val Gly Asn Val Tyr Leu Glu Gly Asn Ala Gly Gln Pro Val Ala			
	325	330		335
	Val Ala Ile Ser Phe Asn Lys Glu Thr Thr Ala Asp Tyr Ser Ile Thr			
	340	345		350
50	Phe Asp Phe Ala Trp Ser Lys Ala Tyr Glu Thr Pro Val Pro Phe Asp			
	355	360	365	
	Thr Ser Ser Met Thr Phe Ser Tyr Ile Ala Gln Glu			
	370	375	380	

<210> 51
<211> 328
<212> PRT
5 <213> adenoviridae

<220>
<221> VARIANT
<222> (1)..(328)
10 <223> /note="Serotype 43 fiber protein"

<400> 51
Asn Ile Pro Xaa Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys
1 5 10 15

15 Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr
20 25 30

Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Gly Leu Thr Val
35 40 45

20 Glu Lys Glu Ser Gly Asn Leu Thr Val Asn Pro Lys Ala Pro Leu Gln
50 55 60

Val Ala Lys Gly Gln Leu Glu Leu Ala Tyr Asp Ser Pro Phe Asp Val
65 70 75 80

25 Lys Asn Asn Met Leu Thr Leu Lys Ala Gly His Gly Leu Ala Val Val
85 90 95

Thr Lys Asp Asn Thr Asp Leu Gln Pro Leu Met Gly Thr Leu Val Val
100 105 110

30 Leu Thr Gly Lys Gly Ile Gly Thr Gly Thr Ser Ala His Gly Gly Thr
115 120 125

Ile Asp Val Arg Ile Gly Lys Asn Gly Ser Leu Ala Phe Asp Lys Asp
35 130 135 140

Gly Asp Leu Val Ala Trp Asp Lys Glu Asn Asp Arg Arg Thr Leu Trp
145 150 155 160

40 Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Met Ser Glu Ala Lys Asp
165 170 175

Ser Lys Leu Thr Leu Ile Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly
180 185 190

45 Ser Val Ser Leu Leu Ala Val Lys Gly Glu Tyr Gln Asn Met Thr Ala
195 200 205

Asn Thr Lys Lys Asn Val Lys Ile Thr Leu Leu Phe Asp Ala Asn Gly
210 215 220

50 Val Leu Leu Ala Gly Ser Ser Xaa Xaa Lys Glu Tyr Trp Asn Phe Arg
225 230 235 240

Ser Asn Asp Ser Thr Val Ser Gly Asn Tyr Glu Asn Ala Val Gln Phe
245 250 255

55 Met Pro Asn Ile Thr Ala Tyr Lys Pro Thr Asn Ser Lys Ser Tyr Ala
260 265 270

Arg Ser Val Ile Phe Gly Asn Val Tyr Ile Asp Ala Lys Pro Tyr Asn
 275 280 285
 5 Pro Val Val Ile Lys Ile Ser Phe Asn Gln Glu Thr Gln Asn Asn Cys
 290 295 300
 10 Val Tyr Ser Ile Ser Phe Asp Tyr Thr Leu Ser Lys Asp Tyr Pro Asn
 305 310 315 320
 Met Gln Phe Asp Val Thr Leu Ser
 325
 15 <210> 52
 <211> 341
 <212> PRT
 <213> adenoviridae
 20 <220>
 <221> VARIANT
 <222> (1)..(341)
 <223> /note="Serotype 44 fiber protein"
 25 <400> 52
 Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Gln
 1 5 10 15
 Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr
 20 25 30
 30 Ile Thr Asn Gly Asn Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu
 35 40 45
 Gln Glu Gly Thr Gly Asp Leu Lys Val Asn Ala Lys Ser Pro Leu Gln
 50 55 60
 35 Val Ala Thr Asn Lys Gln Leu Glu Ile Ala Leu Ala Lys Pro Phe Glu
 65 70 75 80
 40 Glu Lys Asp Gly Lys Leu Ala Leu Lys Ile Gly His Gly Leu Ala Val
 85 90 95
 Val Asp Glu Asn His Thr His Leu Gln Ser Leu Ile Gly Thr Leu Val
 100 105 110
 45 Ile Leu Thr Gly Lys Gly Ile Gly Thr Gly Ser Ala Glu Ser Gly Gly
 115 120 125
 Thr Ile Asp Val Arg Leu Gly Ser Gly Gly Leu Ser Phe Asp Lys
 130 135 140
 50 Asp Gly Asn Leu Val Ala Trp Asn Lys Asp Asp Asp Arg Arg Thr Leu
 145 150 155 160
 Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Lys Ile Asp Gln Asp Lys
 165 170 175
 55 Asp Ser Lys Leu Thr Phe Val Leu Thr Lys Cys Gly Ser Gln Ile Leu
 180 185 190

Ala Asn Met Ser Leu Leu Val Val Lys Gly Lys Phe Ser Met Ile Asn
 195 200 205
 5 Asn Lys Val Asn Gly Thr Asp Asp Tyr Lys Lys Phe Thr Ile Lys Leu
 210 215 220
 Leu Phe Asp Glu Lys Gly Val Leu Leu Lys Asp Ser Ser Leu Asp Lys
 225 230 235 240
 10 Glu Tyr Trp Asn Tyr Arg Ser Asn Asn Asn Val Gly Ser Ala Tyr
 245 250 255
 Glu Glu Ala Val Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Lys Pro
 15 260 265 270
 Pro Thr Pro Pro Thr Asn Pro Thr Thr Pro Leu Glu Lys Ser Gln Ala
 275 280 285
 20 Lys Asn Lys Tyr Val Ser Asn Val Tyr Leu Gly Gly Gln Ala Gly Asn
 290 295 300
 Pro Val Ala Thr Thr Val Ser Phe Asn Lys Glu Thr Gly Cys Thr Tyr
 305 310 315 320
 25 Ser Ile Thr Phe Asp Phe Ala Trp Asn Lys Thr Tyr Glu Asn Val Gln
 325 330 335
 Phe Asp Ser Ser Phe
 340
 30
 <210> 53
 <211> 345
 <212> PRT
 35 <213> adenoviridae
 <220>
 <221> VARIANT
 <222> (1)..(345)
 <223> /note="Serotype 45 fiber protein"
 40 <400> 53
 Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Gln
 1 5 10 15
 45 Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Ala
 20 25 30
 Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Leu Thr Val
 35 40 45
 50 Glu Lys Asp Ser Gly Asn Leu Lys Val Asn Pro Lys Ala Pro Leu Gln
 50 55 60
 Val Thr Thr Asp Lys Gln Leu Glu Ile Ala Leu Ala Tyr Pro Phe Glu
 65 70 75 80
 55 Val Ser Asn Gly Lys Leu Gly Ile Lys Ala Gly His Gly Leu Lys Val
 85 90 95

Ile Asp Lys Ile Ala Gly Leu Glu Gly Leu Ala Gly Thr Leu Val Val
 100 105 110
 5 Leu Thr Gly Lys Gly Ile Gly Thr Glu Asn Leu Glu Asn Ser Asp Gly
 115 120 125
 Ser Ser Arg Gly Val Gly Ile Asn Val Arg Leu Ala Lys Asp Gly Val
 130 135 140
 10 Leu Ala Phe Asp Lys Lys Gly Asp Leu Val Ala Trp Asn Lys His Asp
 145 150 155 160
 Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Thr
 165 170 175
 Ile Asp Gln Glu Arg Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys
 180 185 190
 20 Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Leu Val Val Lys Gly Lys
 195 200 205
 Phe Ser Asn Ile Asn Asn Asn Ala Asn Pro Thr Asp Lys Lys Ile Thr
 210 215 220
 25 Val Lys Leu Leu Phe Asn Glu Lys Gly Val Leu Met Asp Ser Ser Thr
 225 230 235 240
 Leu Lys Lys Glu Tyr Trp Asn Tyr Arg Asn Asp Asn Ser Thr Val Ser
 245 250 255
 30 Gln Ala Tyr Asp Asn Ala Val Pro Phe Met Pro Asn Ile Lys Ala Tyr
 260 265 270
 Pro Lys Pro Ser Thr Asp Thr Ser Ala Lys Pro Glu Asp Lys Lys Ser
 275 280 285
 35 Ala Ala Lys Arg Tyr Ile Val Ser Asn Val Tyr Ile Gly Gly Leu Pro
 290 295 300
 Asp Lys Thr Val Val Ile Thr Ile Lys Phe Asn Ala Glu Thr Glu Cys
 305 310 315 320
 40 Ala Tyr Ser Ile Thr Phe Glu Phe Thr Trp Ala Lys Thr Phe Glu Asp
 325 330 335
 Val Gln Cys Asp Ser Ser Ser Phe Thr
 340 345
 45
 <210> 54
 <211> 340
 50 <212> PRT
 <213> adenoviridae
 <220>
 <221> VARIANT
 <222> (1)..(340)
 55 <223> /note="Serotype 46 fiber protein"

<400> 54
Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys
1 5 10 15

5 Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Ala
20 25 30

Ile Val Asn Gly Asp Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu
35 40 45

10 Gln Glu Gly Asn Leu Thr Val Asp Ala Lys Ala Pro Leu Gln Val Ala
50 55 60

Asn Asp Asn Lys Leu Glu Leu Ser Tyr Ala Asp Pro Phe Glu Val Lys
15 65 70 75 80

Asp Thr Lys Leu Gln Leu Lys Val Gly His Gly Leu Lys Val Ile Asp
85 90 95

20 Glu Lys Thr Ser Ser Gly Leu Gln Ser Leu Ile Gly Asn Leu Val Val
100 105 110

Leu Thr Gly Lys Gly Ile Gly Thr Gln Glu Leu Lys Asp Lys Asp Asp
115 120 125

25 Glu Thr Lys Asn Ile Gly Val Gly Ile Asn Val Arg Ile Gly Lys Asn
130 135 140

Glu Ser Leu Ala Phe Asp Lys Asp Gly Asn Leu Val Ala Trp Asp Asn
145 150 155 160

30 Glu Asn Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Ser Lys
165 170 175

Phe Val Lys Ile Ser Thr Glu Lys Asp Ser Lys Leu Thr Leu Val Leu
180 185 190

35 Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ser Leu Leu Ala Val
195 200 205

Ala Gly Ser Tyr Leu Asn Met Thr Ala Ser Thr Gln Lys Ser Ile Lys
210 215 220

40 Val Ser Leu Met Phe Asp Ser Lys Gly Leu Leu Met Thr Thr Ser Ser
225 230 235 240

Ile Asp Lys Gly Tyr Trp Asn Tyr Arg Asn Lys Asn Ser Val Val Gly
245 250 255

45 Thr Ala Tyr Glu Asn Ala Ile Pro Phe Met Pro Asn Leu Val Ala Tyr
260 265 270

Pro Arg Pro Asn Thr Pro Asp Ser Lys Ile Tyr Ala Arg Ser Lys Ile
50 275 280 285

Val Gly Asn Val Tyr Leu Ala Gly Leu Ala Tyr Gln Pro Ile Val Ile
290 295 300

55 Thr Val Ser Phe Asn Gln Glu Lys Asp Ala Ser Cys Ala Tyr Ser Ile
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 325 330 335

5 Thr Ser Phe Thr
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 <223> /note="Serotype 47 fiber protein"

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 20 25 30

25 Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
 35 40 45

Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
 50 55 60

30 Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly
 65 70 75 80

Gly Leu Thr Leu Gln Glu Gly Thr Gly Asn Leu Thr Val Asn Ala Lys
 85 90 95

35 Ala Pro Leu Gln Val Ala Asp Asp Lys Lys Leu Glu Leu Ser Tyr Asp
 100 105 110

40 Asn Pro Phe Glu Val Ser Ala Asn Lys Leu Ser Leu Lys Val Gly His
 115 120 125

Gly Leu Lys Val Leu Asp Glu Lys Asn Ser Gly Gly Leu Gln Glu Leu
 130 135 140

45 Ile Gly Lys Leu Val Ile Leu Thr Gly Lys Gly Ile Gly Val Glu Glu
 145 150 155 160

Leu Lys Asn Ala Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val Arg
 165 170 175

50 Leu Gly Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Glu Leu Val
 180 185 190

Ala Trp Asn Lys His Asn Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp
 195 200 205

55 Pro Ser Pro Asn Cys Lys Ile Glu Gln Asp Lys Asp Ser Lys Leu Thr
 210 215 220

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Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Met Ala Phe
 225 230 235 240
 5 Gln Val Val Lys Gly Thr Tyr Glu Asn Ile Ser Lys Asn Thr Ala Lys
 245 250 255
 Lys Ser Phe Ser Ile Lys Leu Leu Phe Asp Asp Asn Gly Lys Leu Leu
 260 265 270
 10 Glu Gly Ser Ser Leu Asp Lys Asp Tyr Trp Asn Phe Arg Asn Asp Asp
 275 280 285
 Ser Ile Met Pro Asn Gln Tyr Asp Asn Ala Val Pro Phe Met Pro Asn
 290 295 300
 15 Leu Lys Ala Tyr Pro Asn Pro Lys Thr Ser Thr Val Leu Pro Ser Thr
 305 310 315 320
 Asp Lys Lys Ser Asn Gly Lys Asn Thr Ile Val Ser Asn Leu Tyr Leu
 20 325 330 335
 Glu Gly Lys Ala Tyr Gln Pro Val Ala Val Thr Ile Thr Phe Asn Lys
 340 345 350
 25 Glu Thr Gly Cys Thr Tyr Ser Ile Thr Phe Glu Phe Gly Trp Ala Lys
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 30 Tyr Ile Ala Gln Glu
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 45 1 5 10 15

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Thr Ile Thr Asn Gly Asn Val Ser Leu Lys Val Gly Gly Gly Leu Thr
 50 35 40 45

Leu Gln Glu Gly Thr Gly Asp Leu Lys Val Asn Ala Lys Ser Pro Leu
 50 55 60

Gln Val Ala Thr Asn Lys Gln Leu Glu Ile Ala Leu Ala Lys Pro Phe
 55 65 70 75 80

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Glu Glu Lys Asp Gly Lys Leu Ala Leu Lys Ile Gly His Glu Leu Ala
 85 90 95
 Val Val Asp Glu Asn Leu Thr His Leu Gln Ser Leu Ile Gly Thr Leu
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 Val Ile Leu Thr Gly Lys Gly Ile Gly Thr Gly Arg Ala Glu Ser Gly
 115 120 125
 Gly Thr Ile Asp Val Arg Leu Gly Ser Gly Gly Leu Ser Phe Asp
 130 135 140
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 145 150 155 160
 Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Lys Ile Asp Gln Asp
 165 170 175
 Lys Asp Ser Lys Leu Thr Phe Val Leu Thr Lys Cys Gly Ser Gln Ile
 180 185 190
 Leu Ala Asn Met Ser Leu Leu Val Val Lys Gly Lys Phe Ser Met Ile
 195 200 205
 Asn Asn Lys Val Asn Gly Thr Asp Asp Tyr Lys Lys Phe Thr Ile Lys
 210 215 220
 Leu Leu Phe Asp Glu Lys Gly Val Leu Leu Lys Asp Ser Ser Leu Asp
 225 230 235 240
 Lys Glu Tyr Trp Asn Tyr Arg Ser Asn Asn Asn Asn Val Gly Ser Ala
 245 250 255
 Tyr Glu Glu Ala Val Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Lys
 260 265 270
 Pro Pro Thr Pro Pro Thr Asn Pro Thr Thr Pro Leu Glu Lys Ser Gln
 275 280 285
 Ala Lys Asn Lys Tyr Val Ser Asn Val Tyr Leu Gly Gly Gln Ala Gly
 290 295 300
 Asn Pro Val Ala Thr Thr Val Ser Phe Asn Lys Glu Thr Gly Cys Thr
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 Tyr Ser Ile Thr Phe Asp Phe Ala Trp Asn Lys Thr Tyr Lys Met Ala
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<223> /note="Serotype 49 fiber protein"

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 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
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 10 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
 35 40 45
 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
 50 55 60
 15 Leu Ala Asp Pro Ile Ala Ile Thr Asn Gly Asn Val Ser Leu Lys Val
 65 70 75 80
 Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Asn Leu Lys Val Asn
 85 90 95
 20 Pro Lys Ala Pro Leu Gln Val Ala Thr Asp Asn Gln Leu Glu Ile Ser
 100 105 110
 Leu Ala Asp Pro Phe Glu Val Lys Asn Lys Lys Leu Ser Leu Lys Val
 115 120 125
 Gly His Gly Leu Lys Val Ile Asp Glu Asn Ile Ser Thr Leu Gln Gly
 130 135 140
 30 Leu Leu Gly Asn Leu Val Val Leu Thr Gly Met Gly Ile Gly Thr Glu
 145 150 155 160
 Glu Leu Lys Lys Asp Asp Lys Ile Val Gly Ser Ala Val Asn Val Arg
 165 170 175
 35 Leu Gly Gln Asp Gly Gly Leu Thr Phe Asp Lys Lys Gly Asp Leu Val
 180 185 190
 Ala Trp Asn Lys Glu Asn Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
 195 200 205
 40 Pro Ser Pro Asn Cys Lys Val Ser Glu Glu Lys Asp Ser Lys Leu Thr
 210 215 220
 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ser Leu
 225 230 235 240
 45 Leu Val Val Lys Gly Lys Phe Ala Asn Ile Asn Asn Lys Thr Asn Pro
 245 250 255
 Gly Glu Asp Tyr Lys Xaa Phe Ser Val Lys Leu Leu Phe Asp Ala Asn
 260 265 270
 50 Gly Lys Leu Leu Thr Gly Ser Ser Leu Asp Gly Asn Tyr Trp Asn Tyr
 275 280 285
 Lys Asn Lys Asp Ser Val Ile Gly Ser Pro Tyr Glu Asn Ala Val Pro
 290 295 300
 55 Phe Met Pro Asn Ser Thr Ala Tyr Pro Lys Ile Ile Asn Asn Gly Thr

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	305	310	315	320
	Ala Asn Pro Glu Asp Lys Lys Ser Ala Ala Lys Lys Thr Ile Val Thr			
5	325	330	335	
	Asn Val Tyr Leu Gly Gly Asp Ala Ala Lys Pro Val Ala Thr Thr Ile			
	340	345	350	
10	Ser Phe Asn Lys Glu Thr Glu Ser Asn Cys Val Tyr Ser Ile Thr Phe			
	355	360	365	
	Asp Phe Ala Trp Asn Lys Thr Tyr Lys Asn Val Pro Phe Asp Ser Ser			
	370	375	380	
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	385	390		
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35	 Glu Asp Glu Ser Thr Ser Gln His Pro Phe Ile Asn Pro Gly Phe Ile			
	35	40	45	
	 Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Asn			
	50	55	60	
40	 Cys Leu Thr Pro Leu Thr Thr Gly Gly Pro Leu Gln Leu Lys Val			
	65	70	75	80
	 Gly Gly Gly Leu Ile Val Asp Asp Thr Asp Gly Thr Leu Gln Glu Asn			
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45	 Ile Arg Val Thr Ala Pro Ile Thr Lys Asn Asn His Ser Val Glu Leu			
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	 Ser Ile Gly Asn Gly Leu Glu Thr Gln Asn Asn Lys Leu Cys Ala Lys			
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50	 Leu Gly Asn Gly Leu Lys Phe Asn Asn Gly Asp Ile Cys Ile Lys Asp			
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	 Ser Ile Asn Thr Leu Trp Thr Gly Ile Lys Pro Pro Pro Asn Cys Gln			
55	145	150	155	160

Ile Val Glu Asn Thr Asp Thr Asn Asp Gly Lys Leu Thr Leu Val Leu
 165 170 175
 5 Val Lys Asn Gly Gly Leu Val Asn Gly Tyr Val Ser Leu Val Gly Val
 180 185 190
 Ser Asp Thr Val Asn Gln Met Phe Thr Gln Lys Ser Ala Thr Ile Gln
 10 195 200 205
 Leu Arg Leu Tyr Phe Asp Ser Ser Gly Asn Leu Leu Thr Asp Glu Ser
 210 215 220
 15 Asn Leu Lys Ile Pro Leu Lys Asn Lys Ser Ser Thr Ala Thr Ser Glu
 225 230 235 240
 Ala Ala Thr Ser Ser Lys Ala Phe Met Pro Ser Thr Thr Ala Tyr Pro
 245 250 255
 20 Phe Asn Thr Thr Arg Asp Ser Glu Asn Tyr Ile His Gly Ile Cys
 260 265 270
 Tyr Tyr Met Thr Ser Tyr Asp Arg Ser Leu Val Pro Leu Asn Ile Ser
 275 280 285
 25 Ile Met Leu Asn Ser Arg Thr Ile Ser Ser Asn Val Ala Tyr Ala Ile
 290 295 300
 Gln Phe Glu Trp Asn Leu Asn Ala Lys Glu Ser Pro Glu Ser Asn Ile
 30 305 310 315 320
 Ala Thr Leu Thr Thr Ser Pro Phe Phe Ser Tyr Ile Ile Glu Asp
 325 330 335
 35 Thr Thr Lys Cys Ile Ser Leu Cys Tyr Val Ser Thr Cys Leu Phe Phe
 340 345 350

Asn

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Claims

1. A method for delivering a nucleic acid of interest to a host cell by means of a gene delivery vehicle based on adenoviral material, whereby said gene delivery vehicle delivers the nucleic acid to the host cell by associating with a binding site and/or a receptor present on CAR-negative cells, said binding site and/or receptor being a binding site and/or a receptor for adenovirus subgroups D and/or F.
5
2. Use of a gene delivery vehicle comprising a nucleic acid of interest and comprising adenoviral material involved in binding to a host cell, said material being from a subgroup D and/or F adenovirus, in delivering said nucleic acid of interest to a CAR-negative cell.
10
3. A gene delivery vehicle being a chimaera based on at least two adenoviruses, whereby a cell recognising element of said gene delivery vehicle is based on adenoviral material from a subgroup D and/or F adenovirus, which material confers the capability of infecting CAR negative cells.
15
4. A gene delivery vehicle according to claim 3, wherein said adenoviral material is based on a fiber, a penton and/or a hexon protein of a subgroup D and/or subgroup F adenovirus.
5. A gene delivery vehicle according to claim 3 or 4, further comprising an element from adenovirus 35, responsible for at least partially avoiding an immune response against adenovirus 35.
20
6. A gene delivery vehicle according to any one of claims 3-5, which comprises an element of adenovirus 16 or a functional analogue thereof, which element confers said virus with an enhanced capability to infect smooth muscle cells and/or synoviocytes.
25
7. A gene delivery vehicle according to any one of claims 3-6, comprising a nucleic acid derived from an adenovirus.
8. A gene delivery vehicle according to any one of claims 3-7, comprising a nucleic acid derived from at least two different adenoviruses.
30
9. A gene delivery vehicle according to claim 7 or claim 8, wherein said nucleic acid comprises at least one sequence encoding a capsid protein comprising at least a tissue tropism determining fragment of a subgroup D and/or subgroup F adenovirus capsid protein.
- 35 10. A gene delivery vehicle according to any one of claims 7-9, wherein said nucleic acid derived from adenovirus is modified such that the capacity of said nucleic acid to replicate in a target cell has been reduced or disabled.
11. A gene delivery vehicle according to any one of claims 7-10, wherein said nucleic acid derived from adenovirus is modified such that the capacity of a host immune system to mount an immune response against adenovirus proteins encoded by said nucleic acid derived from adenovirus has been reduced or disabled.
40
12. A gene delivery vehicle according to anyone of claims 7-11, comprising a minimal adenovirus vector or an integrating adenovirus such as an Ad/AAV chimaeric vector, a retro-adenovirus or a transposon-adenovirus.
- 45 13. A gene delivery vehicle according to anyone of the claims 1-12, further comprising at least one non-adenovirus nucleic acid.
14. A gene delivery vehicle according to anyone of claims 7-13, wherein said nucleic acid derived from adenovirus is produced by welding together through homologous recombination two nucleic acid molecules comprising partially overlapping sequences wherein said overlapping sequences allow essentially only one homologous recombination which leads to the generation of a physically linked nucleic acid comprising at least two functional adenovirus inverted terminal repeats, a functional encapsulation signal, a nucleic acid of interest, or functional parts, derivatives and/or analogues thereof.
50
- 55 15. A cell for the production of a gene delivery vehicle according to anyone of the claims 3-14, comprising means for the assembly of said gene delivery vehicle wherein said means includes a means for the production of an adenovirus capsid protein, wherein said capsid protein comprises at least a receptor and/or binding site binding fragment of a subgroup D and/or subgroup F adenovirus capsid protein.

16. A cell according to claim 15, wherein said cell is or is derived from a PER.C6 cell (ECACC deposit number 96022940).

5 17. The use of a gene delivery vehicle according to anyone of the claims 1-14 as a pharmaceutical.

18. A receptor and/or a binding site for adenoviruses type D and/or F, present on or associated with CAR negative cells.

10 19. A receptor and/or a binding site according to claim 18, present on K562 cells, amniotic fluid cells and/or primary fibroblast cells.

20 20. A capsid protein derived from a subgroup D and/or a subgroup F adenovirus or a functional part, derivative and/or analogue thereof.

15 21. A capsid protein according to claim 20, wherein said protein is a fiber protein.

22. An isolate and/or recombinant nucleic acid encoding a capsid protein according to claim 20 or claim 21.

20 23. An isolate and/or recombinant nucleic acid according to claim 22, wherein said nucleic acid comprises a sequence as depicted in figure 7.

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Figure 1

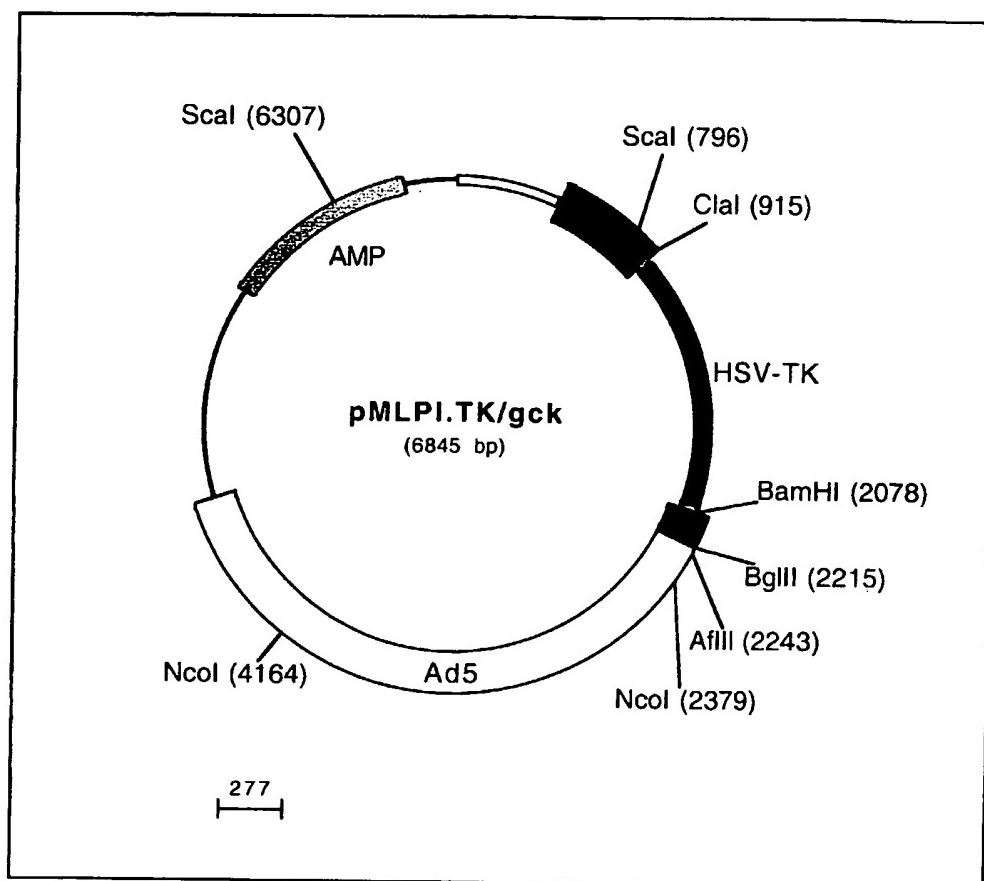


Figure 2

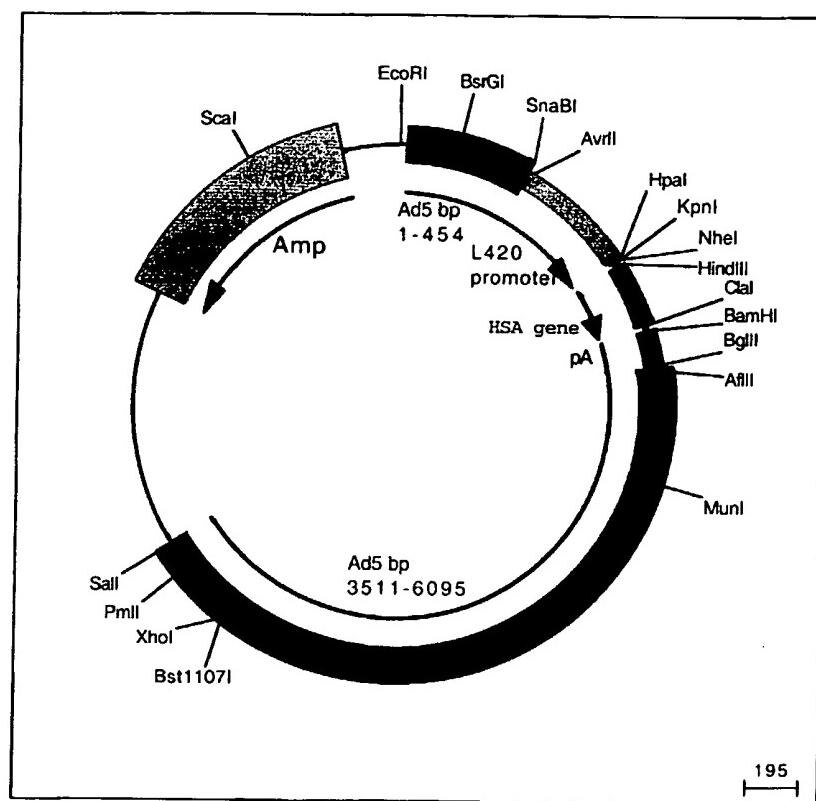


Figure 3

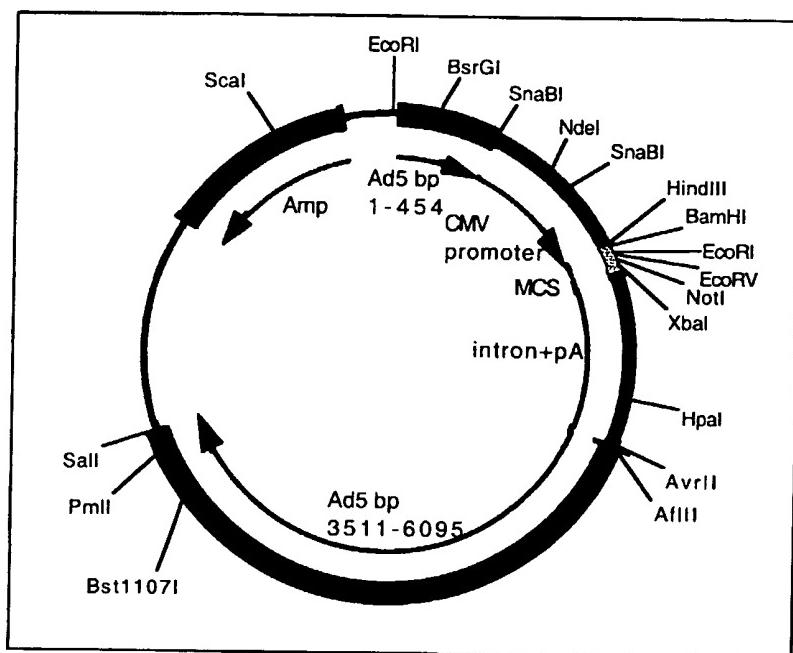


Figure 4

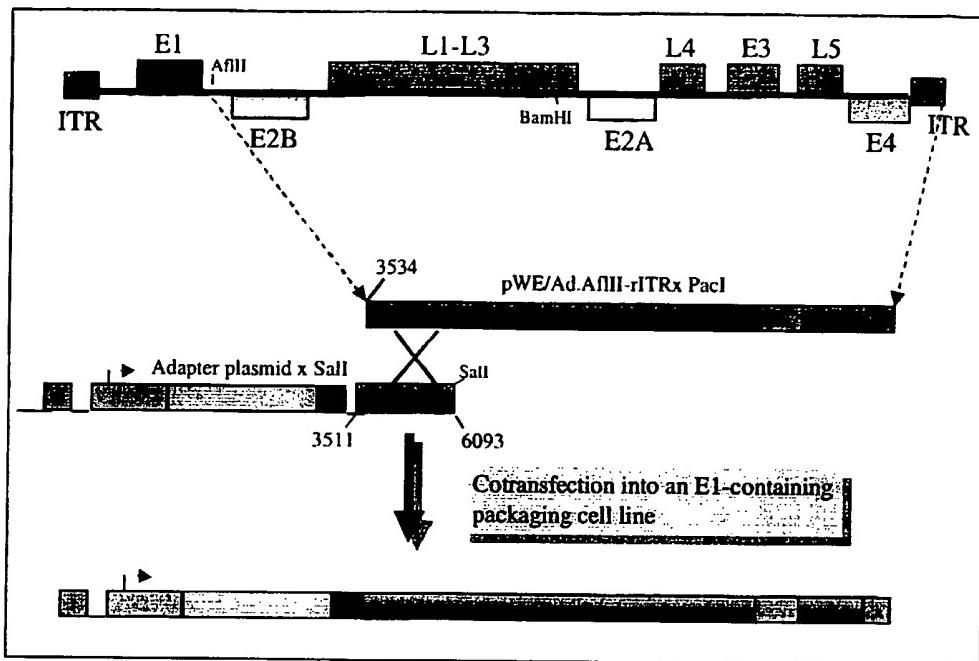


Figure 5

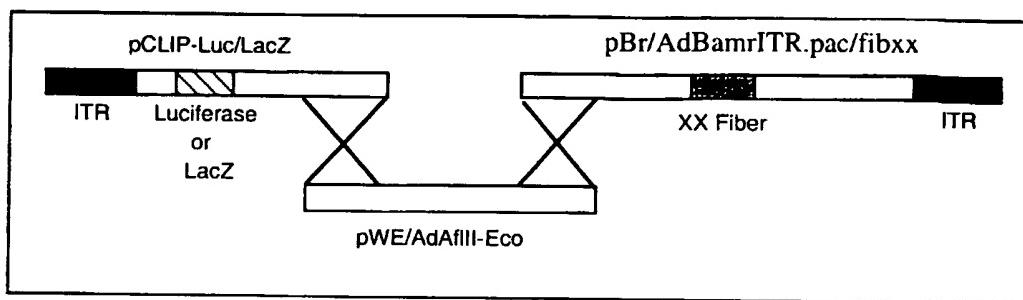


Figure 6

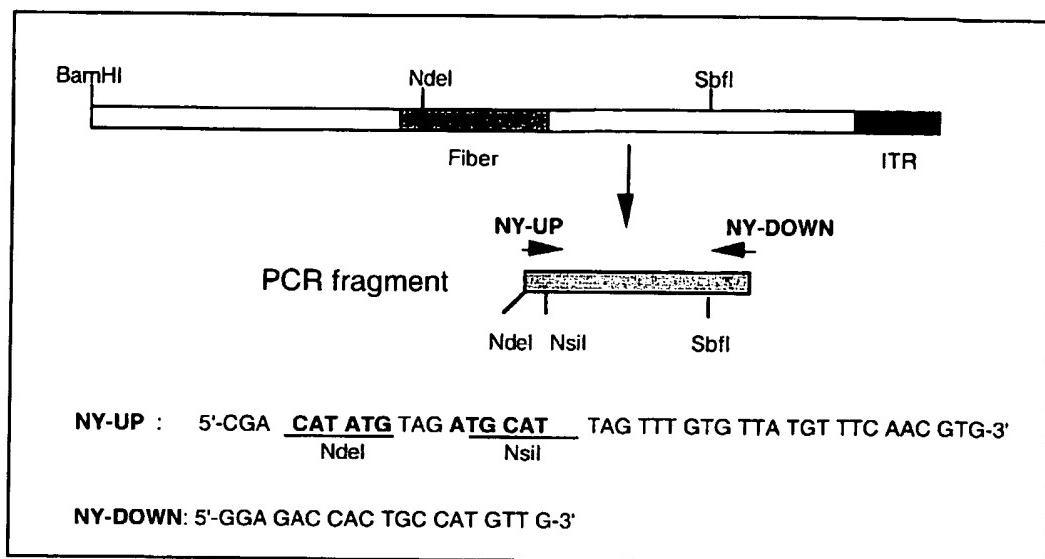


Figure 7:

1.1: Serotype 8 fiber protein

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ALDAPFDVIDNKLTLLAGHGLSIITKETSTLPGLVNTLVVLTGKGIGTDLSNNGN
ICVRVGEGGGLSFNDNGDLVAFNKKEDKRTLWTPDTSPNCRIDQDKDSKLT
LTKCGSQILANVSLIVVAGRYKIINNNTNPALKGFTIKLLFDKNGVLMESNLGK
YWFRNQNSIMSTAYEKAIGFMPNLVAYPKPTGSKKYARDIVYGNIYLGGKPH
QPVTIKTTFNQETGCEYSITFDFSWAKTYVNVEFETTSFTFSYIAQE.

1.2: Serotype 9 fiber protein

SCSCPSAPТИFMLLQMKRARPSEDTNPVYPYGYARNQNIPFLTPPFVSSDGFQ
NFPPGVLSKLADPIAVNGNVSLKVGGGLTLQDGTLKLTNVADPPLQLTNNKL
GIALDAPFDVIDNKLTLLAGHGLSIITKETSTLPGLINTLVVLTGKGIGTESTDNGG
SVCVRVGEGGGLSFNDNGDLVAFNKKEDKRTLWTPDTSPNCRIDQDKDSKLT
VLTCKCGSQILANVSLIVVAGKYKIINNNTQPALKGFTIKLLFDENGVLMESNLGK
SYWNFRNENSIMSTAYEKAIGFMPNLVAYPKPTAGSKKYARDIVYGNIYLGGKPH
DQPVTIKTTFNQETGCEYSITFDFSWAKTYVNVEFETTSFTFSYIAQE.

1.3: Serotype 13 fiber protein

XXXXXSAPТИFMLLQMKRARSSXDTNPVYPYGYARNQNIXXTPPFXSDGF
KNFPPGVLSKLADPITIANGDVSLKVGGGLTLQEGSLTVDPKAPLQLANDKKLE
LVYDDPFEVSTNKLSLKVGHGLVKLDDKSAGGLKDLIGKLVVLTGKGIGIENLQ
NDDGSSRGVGVINVRLGTDGGLSFDRKGELVAWRKDDRTLWTPDPSPNCKA
ETEKDSKLTVLTKCGSQILATVSIIVLKGKYEFVKKETEPKSFDVKLLFDKGVL
LPTSMLSKEYWNYRSYDNNIGTPYENAVPFMPNLKAYPKPTKTASDKAENKISS
AKNKIVSNFYFGGQAQPGTIIKFNEEIDETCAYSITFNFGWGKVYDNPFPFDTS
FTXSYIAQE.

1.4: Serotype 14 fiber protein

HPFINPGFISPNGFTQSPDGVLTLKCLTPLTTGGSQLLKVGGLTVDDTDGLQ
NIGATTPLVKTGHSIGLSLGAGLGTDENKLCTKLGEGLTFNSNNICIDDNINTLWT
GVNPTEANCQMMDSSESNDCKLILTLVKTGALVTAFFVYVIGVSNNFNMLTTYRN
INFTAELFFDSAGNLLTSSLKTPLNHKGQTWLLVPLLMLKVSCPACQLLISIIIL
EKNKTTFTELVTTQLVITLLFPLTISVMLNQRAIRADTSYCIRITWSWNTGDAPEG
QTSATTLVTS

1.5: Serotype 20 fiber protein

IQNIPFLTPPFVSSDGLQNFPPGVLSKLADPIAVNGNVSLKVGGGITVEQDSQL
IANPKAPLQVANDKLELSYAYPFETSANKLSLKVGQGLKVLDEKDSGGLQNL
KLVVLTGKGIGVEELKNPDNTNRGVGINVRLGKDGLSFNKNGELVAWNKHND

Figure 7 cont.

TGTLWTPPDPSNCKIEVKDSLTLVLTCKGSQILATMAFQVVKGTYENISKNT
AKNSFSIKLLFDDNGKLLEGSSLDKDWNFRSDSIIIPNQYDNAVPFMPNLKAYP
KPSTVLPSTDKNNGKNTIVSNLYLEGKAYQPVAVTITFNKEIGCTYSITFDGFWA
KTYDVPIPFDSSFT

1.6: Serotype 23 fiber protein

QNIPFLTPPFVSSDGFQNFPPGVSLKLADPIAITNGDVS LKVGGGLTVEQDSGNL
KVNTKAPLQVAADKQLEIALADPFEVSKGRLGIKAGHGLKVIDNSISGLELVGT
LVVLTGHGIGTENLLNNDGSSRGVGIVNRGLKDGGLSFDKKGDLVAWNKKYDT
RTLWTPPDPSNCKVIEAKDSLTLVLTCKGSQILANMSLILKGTYEYISNAIAN
KSFTIKLLFNDKGVLMDGSSLKD YWNYKSDDSVMSKA YENA VPFMPNLKAYP
NPTTSTTNPSTDKNNGKNAIVSNVYLEGRAYQPVAITITFNKGCTYSMTDF
GWSK VYNDPIPFDTSSLT

1.7: Serotype 24 fiber protein

SCSCPSA PTIFM LLQM K RARP SEDTFNPVYPYGYARNQNI PFLTPPFVSSDGFQ
NFPPGVLSKLADPIAITNGDVS LKVGGGLTVEKDSGNLKVNPKAPLQVTTDKQL
EIALA YPFEVSGKLGKAGHGLKVIDKIAGLEGLAGTLVVL TGKGIGTENLENS
DGSSRGVGIVNR LA KDGGLSF DKKGDLVAWNKHDDRRTLWTPPDPSNCTIDQ
ERDSKLTLVLTCKGSQILANVSLVVKGKFSNINNNPTDKKITVKLLFNEKG
LMDSSLKKEYWNYRNDNSTVSQA YDNAVPFMPNI A YPKPTTDTSAKPEDKK
SAAKRYIVSNVYIGGLPDKTVVITIKFNAETECAYSITFEFTWAKTFEDVQFDSS
TFSYIAQE.

1.8: Serotype 25 fiber protein

SCSCPSA PTIFM LLQM K RARP SEDTFNPVYPYGYARNQNI PFLTPPFVSSDGFQ
NFPPGVLSKLADPITISNGDVS LKVGGGLTVEQDSGNLSVNPKAPLQVGTDKKL
ELALAPPFNVKDNKL DLLVGDG LKVIDKSISXLPGLLNYL VVL TGKGIGNEELKN
DDGSNKVGGLCVRIGEGGGLTFDDKGYLVAWNKKHDIRTLWTTLDPSNCRID
VDKDSKLTLVLTCKGSQILANVSLVVKGRFQNLNYKTNP NLPKTFTIKLLFDEN
GILKDSSNLDK NYWNYRNGNSILA EQYKNAVG FMPNLA AYPKSTT QSKLYAR
NTIFGNIY LDSQAYNPVVI KITFNQEA DSA YSITLN YSWGKD YENIPFDS

1.9: Serotype 27 fiber protein

IPFLTPPFVSSDGFKNFPPGVSLKLADPITITNGDVS LKVGGGLVVEKESGKLSV
DPKTPLQVASDNKLELSYNAPFKVENDKSLDVHGGLK VIGNEVSSLPGLINKLV
VLTGKGIGTEELKEQNSDKIIGVGIVNRARGGLSFNDG YLVAWNPKYDTRTLW
TTPDTSPNCKMLTKKDSKLTLTKCGS QILGNV SLLAVSGKYL NMTKDETGVKI
ILLFDRNGVLMQESSLDKEYWNYRNDNNVIGTPYENAVGFMPNLVAYPKPTSA
DAKNYSRSK IISNVY LKGLIYQPVIIASFNQETTNGCVY SISFDFTCSKD YTGQQF
DVT SF

1.10: Serotype 28 fiber protein

SCSCPSA PTIFM LLQM K RARP SEDTFNPVYPYGYARNQNI PFLTPPFVSSDGFQ
NFPPGVLSKLADPITIANGDVS LKGGLTVEKESG NLTVNPKAPLQV ASGQLE
LAYYSPFDVKNNMLTLKAGHGLAVVTKDNTDLQPLMGT L VVL TGKGIGTGTSA

Figure 7 cont.

HGGTIDVRIGKNGSLAFDKNGDLVAWDKENDRRTLWTPDTSPNCKMSEVKDS
KLTLLTKCGSQLGSVSLAVKGEYQNMATASTNKNVKITLLFDANGVLLEGSSL
DKEYWNFRNNNDSTVSGKYENAVPFMPNITA YKPVNSKSYARSHIFGNVYIDAKP
YNPVVIKISFNQETQNNCVYSISFDYTCSKEYTGMQFDVTSTFSYIAQE.

1.11: Serotype 29 fiber protein

QNIPFLTPPFVSSDGFKNFPPGVLSKLADPIAITNGDVS LKVGGGLTVEQDSGNL
SVNP KAPLQVGTDKKLELALAPPFDVRDNKLAILVG DGLKVIDRSISDLPG LNY
LVVLTGKGIGNEELKNDGSNKGVGLCVRIGEGGGLTFDDKGYLVA WNNKHDI
RTLWTLDPSPNCKIDIEKDSKTL VLT KCGSQILANVSLIIVNGKF KILNNKTDP
LPKS FNIKLLFDQNGVLLENS NIEKQYLNFRSGDSILPEPYKNAIGFMPNLLAYAK
ATT DQSKIYARNTIYGNIYLDNQPYNPVVIKITFNNEADSAYSITFNYSWTKDYD
NIPFDSTSFTS

1.12: Serotype 30 fiber protein

SCSCPSA PTIFM LLQM KRARP SXT FNPV PYGYARN QNIP FXT PPFV SDG FK
NFPPGVLSKLADPIAITNGDVS LKVGGGLTVEQDSGNL SVNX KAPLQVGTDKK
LELALAPPFDVRDNKLAILVG DGLKVIDRSISDLPG LNY LVVXTGKGIGNEELK
NDGSNKGVGLCVRIGEGGGLTXDDKGYLVA WNNKHDIRTLWTLDPSPNCKI
DIEKDSKTL VLT KCGSQILANVSLIIVNGKF KILNNKTDP SLPKSF NIKLLFDQNG
VLLENS NIEKQYLNFRSGDSILPEPYKNAIGFMPNLLAYAK ATT DQSKIYARNTIY
GNIYLDNQPYNPVVIKITFNNEADSAYSITFNYSWTKDYDNIPFDSTSFTFSYIAQE

1.13: Serotype 32 fiber protein

SCSCPSA PTIFM LLQM KRARP SEDTFNPV PYGYARN QNIP FLT PPFVSSDG FQ
NFPPGVLSKLADPIAITANGVSLKVGGGLTLEQD SGK LIVNP KAPLQV AND KLE
LSYADPFET SANKLSLKVGHGLKVLDEKNAGGLKDLIGTLVVL TGKGIGVEELK
NADNTNRGVGINVRLGKDGGLSFDKKGD LVAWNK HDDRRTLWTPDPSPNCTI
DEERDSKTL VLT KCGSQILANVSLVVKGKFSNINNNTNPTDKKITV KLLFNEK
GVLMDSSSLKKEYWNYRNDNSTVSQAYDNAVPFMPNIKAYPKPTTDSAKPED
KKSAAKRYIVSNVYIGGLPDKTVVITIKLNAETESA YSMTF EFTWAKTFENLQFD
SSSFTFSYIAQE.

1.14: Serotype 33 fiber protein

SCSCPSA PTIFM LLQM KRARP SEDTFNPV PYGYARN QNIP FLT PPFVSSDG FK
NFPPGVLSKLADPIITNGDVS LKVGGGLTLEQEGSLTVNP KAPLQL AND KKLE
VYDDPFEVSTNKL SLKVGHGLKVLDDKSAGGLQDLIGKLVVL TGKGIGIENLQN
DDGSSRGVGINVRLGTDGGLSFDRKGELVAWNK HDDRRTLWTPDPSPNCKAE
TEKDSKTL VLT KCGSQILATVSIIVLKGKYEFVKKETEPKSF DVKLLFD SKGVLL
PTSNLSKEYWNYRSYDNNIGTPYENAVPFMPNLKAYPKPTKTASDKAENKISSA
KNKIVSNFYFGGQAYQPGTIUKFNEEIDETCAYSITFNFGWGKVYDNPFPFDTSF
TFSYIAQE.

1.15: Serotype 34 fiber protein

Figure 7 cont.

SCSCPASPTIFMLLQMKRARPSEDTFPVYPYEDESTSQHPFINPGFISPNGFTQ
SPDGVLTLKCLTPLTTGGSQLKVGGLTVDDTDGTLQKNIRATTPITKNNSV
ELTIGNGLETQHNKLCALKGNGLKFNNGDICIKDSINTLWTGINPPNCQIVENTN
TNDGKLTFLVVKNGGLVNGYVSLVGVSDTVNQMFTQKTANIQRLYFDSSGNL
LTDESDLKIPLKNKSSTATSETVASSKAFMPSTAYPFNTTRDSENYIHGICYYM
TSYDRSLFPLNISIMLNSRMISSNVAYAIQFEWNLNASESPEKQHMTLTTSPFFSY
IIEDDN.

1.16: Serotype 35 fiber protein

SCSCPASPTIFMLLQMKRARPSEDTFPVYPYEDESTSQHPFINPGFISPNGFTQ
SPDGVLTLKCLTPLTTGGSQLKVGGLTVDDTDGTLQENIRATAPITKNNSV
ELSIGNGLETQNNKLCALKGNGLKFNNGDICIKDSINTLWTGINPPNCQIVENTN
TNDGKLTFLVVKNGGLVNGYVSLVGVSDTVNQMFTQKTANIQRLYFDSSGNL
LTEESDLKIPLKNKSSTATSETVASSKAFMPSTAYPFNTTRDSENYIHGICYYM
TSYDRSLFPLNISIMLNSRMISSNVAYAIQFEWNLNASESPESNIMTLTTSPFFSYI
TEDDN.

1.17 Serotype 36 fiber protein

SCSCPASPTIFMLLQMKRARPSEDTFPVYPGYARNQNIPFLTPPFVSSDGFK
NFPPGVLSLKLADPIAVNGDVSLKVGGGLTVEQDSGKLKVNPKIPQLQVVNDQLE
LATDKPKIENNKLALDVGHGLKVIDKTISDLQGLVGKLVVLTVGIGTETLKDK
NDKVIGSAVNVRGKDGGLDFNKKGLVAWNRYDDRRTLWTPDPSPNCKVS
EAKDSKLTFLVTKCGSQILASVALLIVKGKYQTISESTIPKDQRNFSKLMFDEKG
KLLDKSSLKEYWNFRSNDSVVGTAYDNAVPFMPNLKAYPKNTTSSTNPDDKI
SAGKKNIVSNVYLEGRVYQPVALTVKFNSENDCAYSITFDFVWSKTYESPVAFD
SSSFTFSYIAQE.

1.18 Serotype 37 fiber protein

SCSCPASPTIFMLLQMKRARPSEDTFPVYPGYARNQNIPFLTPPFVSSDGFK
NFPPGVLSLKLADPITITNGDVSLKVGGGLTLQDGSLTVNPKAPLQVNTDKKEL
AYDNPFESSIONKLSLKVGHGLKVLDEKSAAGLKDLIGKLVVLTGKGIGTENLEN
TDGSSRGIGINVRAEGLTFDNDGYLVAWNPKYDLRTLWTPDTSPNCTIAQDK
DSKLTFLVTKCGSQILANVSLIVVAGKYHIINNKTNPKIKSFTIKLLFNKNGVLLD
NSNLGKAYWNFRSGNSNVSTAYEKAIGFMPNLVAVKPSNSKKYARDIVYGNIY
LGGKPDQPGVIKTFNQETGCEYSITFNFSWSKTYENVEFETTSFTFSYIAQE.

1.19 Serotype 38 fiber protein

SCSCPASPTIFMLLQMKRARPSEDTFPVYPGYARNQNIPFXTPPFVXSDGFQ
NFPPGVLSLKLADPITIANGVSLKVGGGLTLEQDSGKLIVNXKAPLQVANDKLE
LSYADPFETSANKLSLKVGHGLKVLDEKNAGGLKDLIGTLVVLTGKGIGVEELK
NADNTNRGVGINVRGKDGGLSFDDKGDXVAWNKHDDRRTLWTPDPSPNCTI
DEERDSKLTFLVTKCGSQILANVSLVVKGKFSNINNNNTNPTDKKITVKLLFNEK
GVLMDSSSLKKEYWNYRNDNSTVSQAYDNAVPFMPNIKAYPKPTTDTSAKPED
KKSAAKRYIVSNVYIGGLPDKTVVITIKLNAETESAYSMTFEFTWAKTFENLQFD
SSSFTFSYIAQE.

Figure 7 cont.

1.20 Serotype 39 fiber protein

IRISPSSLPLSPPMDSKTSPLGCYHSNWLTQSPSPGMGSHSRWEGGSPWQEGTG
DLKVNAKSPLQVATNKQLEIALAKPFEEKDGKLALKIGHGLAVVDENHTHLQSL
IGTLVILTGKGIGTGRAESGGTIDVRLGSGGLSFKDGNLVAWNKDDDRRTLW
TTPDPSPNCKIDQDKDSKLTFLTKCGSQILANMSLLVVKGKFMSINNKVNGETD
DYKKFTIKLLFDEKGVLKDSSLKEYWNYRSNNNVGSAYPEAVGFMPSTTA
YPKPPTPTNPTTLEKSQAKNKYVSVNLGGQAGNPVATTFSFNKETGCTYSIT
FDFAWNKTYENVQC.

1.21: Serotype 42 fiber protein

SCSCPSA PTIFMLLQMKRARPSEDTFNPVPPYCYARNQNIPFLTPPFVSSDGFK
NFPPGVLSLKLANPIATNGDVSLKVGGLTLQDGTKLTIDTKTPLQVANNKLE
LA FDAPLYEKNGKLALKTGHGLAVLTKDIGIPELIGSLVILTGKGIGTGTVAGGGT
IDVRLGDDGGLSFDDKKGDLVAWNKNDRRTLWTTPDPSNCRVSEDKDSKLT
LTKCGSQILASFSLVVXGTYTTVDKNTTNQFSIKLLFDANGKLKSESNLGYW
NYRSDNSVSVTPYDNAVPFMPNTTAYPKIINSTTDPENKSSAKKTIVGNVYLEG
NAGQPVAVAISFNKETTADYSITFDFAWSKAYETPVPDFTSSMTFSYIAQE.

1.22: Serotype 43 fiber protein

NIPXLTPPFVSSDGFKNFPPGVLSLKLADPITITNGDVSLKVGGLTVEKESGNLT
VNPKAPLQVAKGQLEAYDSPFDVKNNMLTLKAGHGLAVVTKDNTDLQPLMG
TLVVLTKKGIGTGTSAHGTIDVRIGKNGSLAFDKDGDLSAWDKENDRRTLWT
TPDTSPNCKMSEAKDSKLTLLTKCGSQILGSVSLLAVKGEYQNMANTKKNVKI
TLLFDANGVLLAGSSXXKEYWNFRSDSTVSGNYENA VQFMPNITA YKPTNSKS
YARSVIFGNVYIDAKPYNPVVIKISFNQETQNNCVYSISFDYTLSKDYPNMQFDV
TLS

1.23: Serotype 44 fiber protein

NIPFLTPPFVSSDGQFNFPFGVLSLKLADPITITNGNVSLKVGGLTLQEGTGDLK
VNAKSPLQVATNKQLEIALAKPFEEKDGKLALKIGHGLAVVDENHTHLQSLIGTL
VILTGKGIGTGSAESGGTIDVRLGSGGLSFKDGNLVAWNKDDDRRTLWTTPD
PSNCVSKIDQDKDSKLTFLTKCGSQILANMSLLVVKGKFMSINNKVNGETDDYKK
FTIKLLFDEKGVLKDSSLKEYWNYRSNNNVGSAYPEAVGFMPSTTA YPKPP
TPPTNPTTLEKSQAKNKYVSVNLGGQAGNPVATTFSFNKETGCTYSITFDFA
WNKTYENVQFDSSF

1.24: Serotype 45 fiber protein

NIPFLTPPFVSSDGQFNFPFGVLSLKLADPIAITNGDVSLKVGGLTVEKDSGNLK
VNPKAPLQVTTDKQLEIALAYPFEVNGKLGKAGHGLKVIDKIAGLEGLAGTLV
VLTGKGIGTENLENSDGSSRGVGINVRLAKDGVLAFDKKGDLVAWNKHDDRRT
LWTTPDPSNCTIDQERDSKLTLLTKCGSQILANVSLLVVKGKFMSINNNANPT
DKKITVKLLFNEKGVLMDSSLKKEYWNYRNDNSTVSQAYDNAVPFMPNIKAY
PKPSTDTSAKPEDKSAAKRYIVSNVYIGGLPDKTVVITIKFNAETECAYSITFEFT
WAKTFEDVQCDSSSFT

1.25: Serotype 46 fiber protein

Figure 7 cont.

NIPFLTPPFVSSDGFKNFPPGVSLKLADPIAIVNQDVSLKVGGGLTLQEGNLTVD
AKAPLQVANDNKLELSYADPFEVKDTKLQLKVGHGLKVIDEKTSGLQSLIGNL
VVLTGKGIGTQUELKDKDDETKNIGVGIVRIGKNESLAFDKDGNLVAWDNENDR
RTLWTPDTSSKFVVKISTEKDSKLTVLTKCGSQILASVLLAVAGSYLNMTAST
QKSIVSLSMFDSKGLLMTSSIDKGYWNYRNKNSVVGTAAYENAIPFMPNLVAYP
RPNTPDSKIYARSKIVGNVYLAGLAYQPIVITVSFNQEKDASCAYSITFEFAWNKD
YVGQFDTSFT

1.26 Serotype 47 fiber protein

SCPSAPTIFMLLQMKRARPSEDTFPVVPYGYARNQNIPFLTPPFVSSDGFKNF
PPGVSLKLADPITITNGDVSLSKVGGGLTLQEGTGNLTNVNAKAPLQVADDKKLE
LSYDNPFEVSANKLSLKVGHGLKVLDEKNSGGLQELIGKLVLTGKGIGVEELKN
ADNTNRGVGINVRLGKDGGLSFDKKGELVAWNKHNDRTLWTPDPSPNCKIE
QDKDSKLTVLTKCGSQILATMAFQVVKGTYENISKNTAKKSFSIKLLFDDNGKL
LEGSSLDKDYWNFRNDDSIMPNQYDNAVPFMPNLKAYPNPKTSTVLPSTDKKSN
GKNTIVSNLYLEGKAYQPVAVTITFNKETGCTYSITFEFGWAKTYDVPIPFDSSSF
TFSYIAQE.

1.27: Serotype 48 fiber protein

SDIPFLTPPFVSSDGFQNFPPGVSLKLADPITITNGVSLKVGGGLTLQEGTGDLK
VNAKSPLQVATNKQLEIALAKPFEEDGKLALKIGHELAVVDENLTHLQSLIGTL
VLTGKGIGTGRAESGGTIDVRLSGGGLSFDKGNLVAWNKDDDRRTLWTPD
PSPNCKIDQDKDSKLTFLTKCGSQILANMSLLVVKGKFSMINNKVNGTDDYKK
FTIKLLFDEKGVLKKDSSLKEYWNYRSNNNNVGSAYEEAVGFMPSTTAYPKPP
TPPTNPTTPLEKSQAKNKYVSVYLGGQAGNPVATTVSFNKETGCTYSITFDFA
WNKTYKMAFIPRFNF

1.28: Serotype 49 fiber protein

SCSCPSAPTIFMLLQMKRARPSEDTFPVVPYGYARNQNIPFLTPPFVSSDGFQ
NFPPGVSLKLADPIAITNGVSLKVGGGLTVEQDSGNLKVNPKAPLQVATDNQ
LEISLADPFEVKNNKLSLKVGHGLKVIDENISTLQGLLGNLVVLTMGIGTEELK
KDDKIVGSAVNVRLGQDGGLFDKKGDLVAWNKENDRRTLWTPDPSPNCKVS
EEKDSKLTVLTKCGSQILASVLLVVKGKFSMINNKVNGTDDYKK
NGKLLTGSSLGDNYWNYKNKDSVIGSPYENAVFMPNSTAYPKIINNGTANPED
KKSAAKKTIVTNVYLGGDAAKPVATTISFNKETESNCVYSITFDAWNKTYKNV
PFDSLTSFTSYIAQE.

1.29.: Serotype 51 Fiber protein

SCSCPSAPTIFMLLQMKRARPSEDTFPVVPYEDESTSQHPFINPGFISPNGFTQ
SPDGVLTLNCLTPLTTGGPLQLKVGGGLIVDDTDGTLQENIRVTAPITKNNHSV
ELSINGLETQNNKLCALKGNGLKFNNNGDICIKDSINTLWTGIKPPNCQIVENTD
TNDGKLTIVLVNGGLVNGYVSLVGVSFTVNQMFHQKSAIQRLYFDSSGNLL
TDESNLKIPLKNKSSTATSEAATSSKAFFPSTTAYPFNTTTRDSENYIHGICYYMT
SYDRSLVPLNISIMLNSRTISSNVAYAIQFEWNLNAKESPESNIATLTTSPFFSYIIIE
DTTKCISLCYVSTCLFFN

Figure 8:

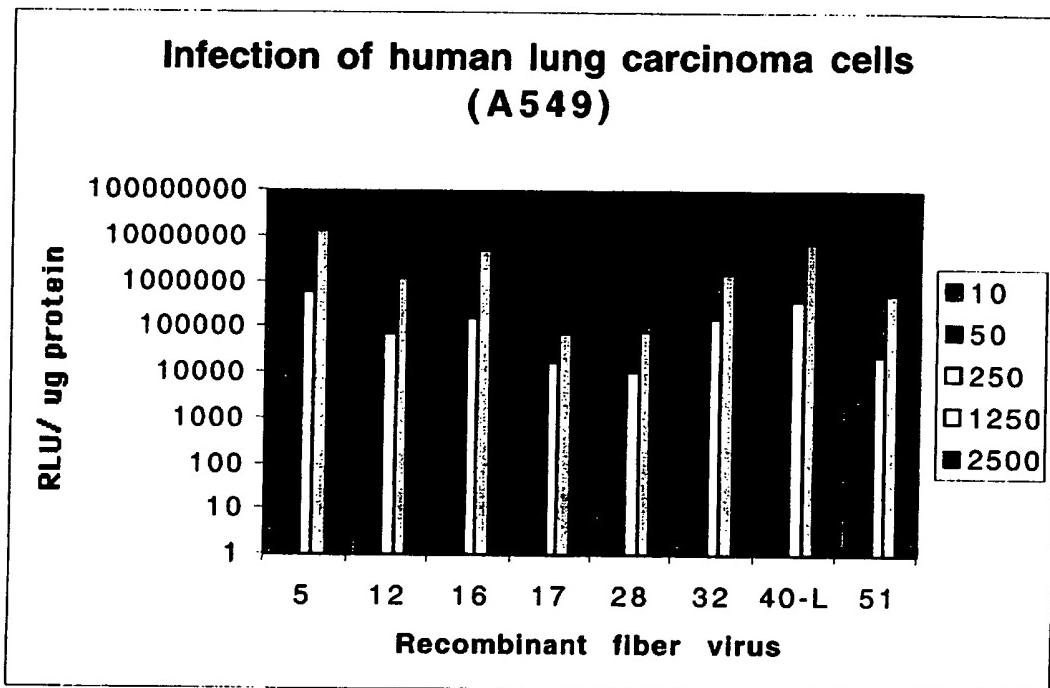


Figure 9

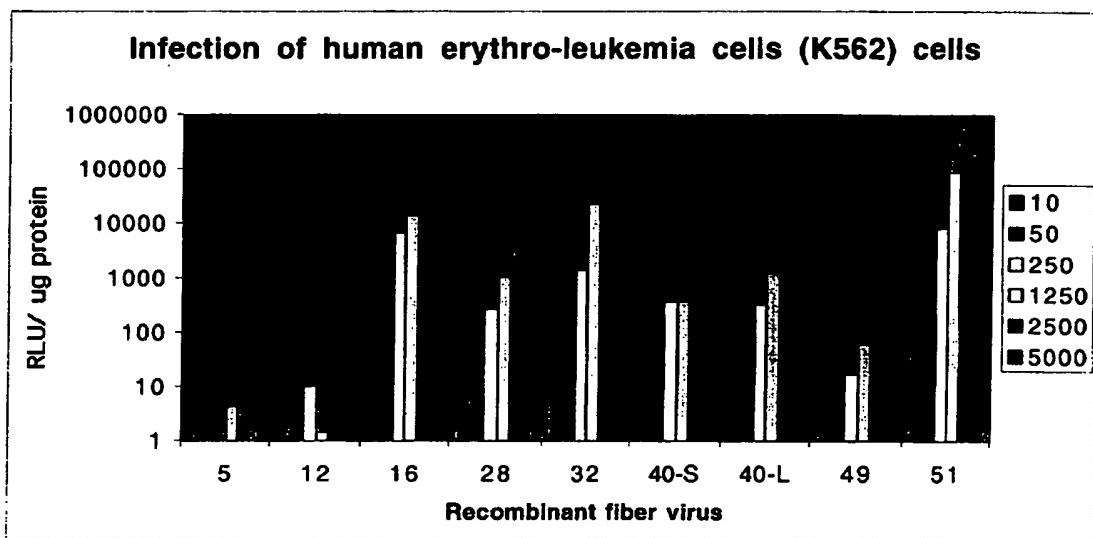


Figure 10

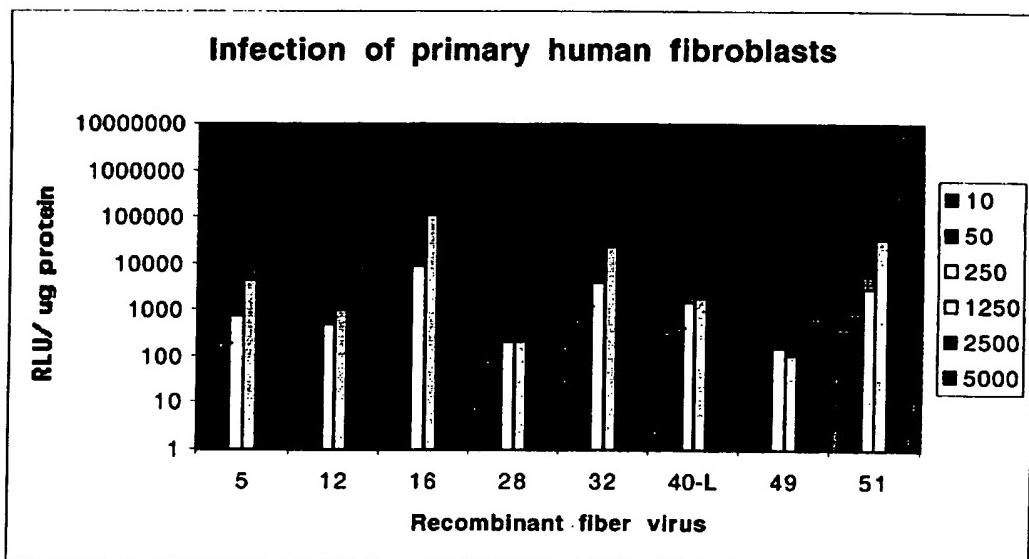


Figure 11

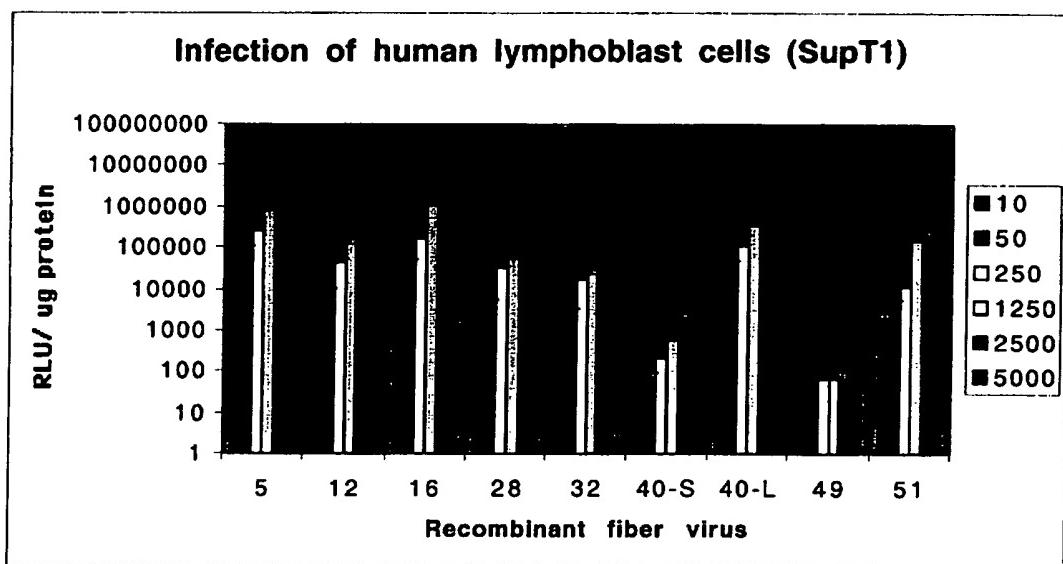


Figure 12

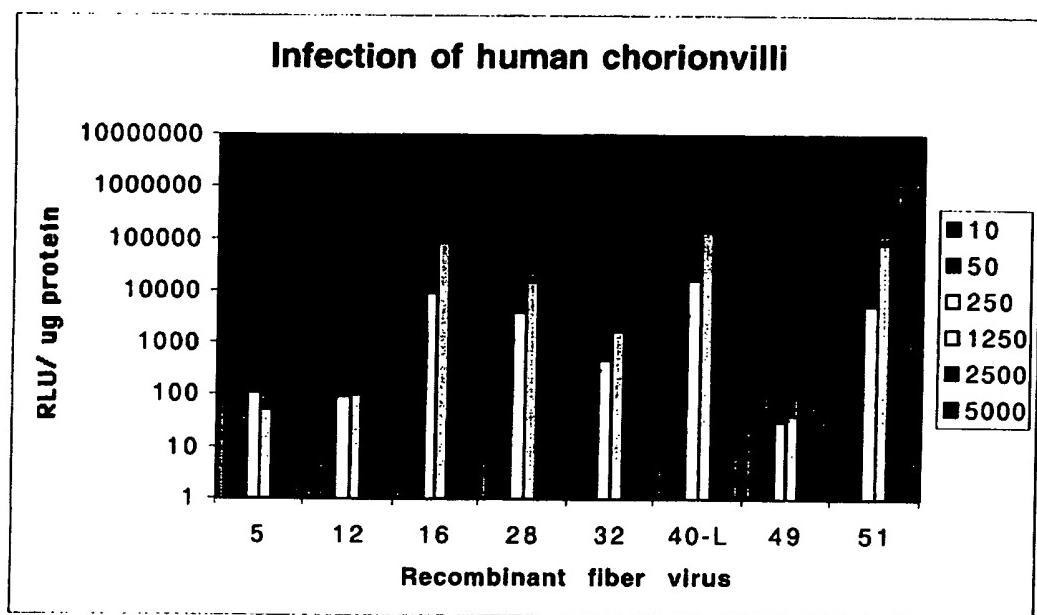
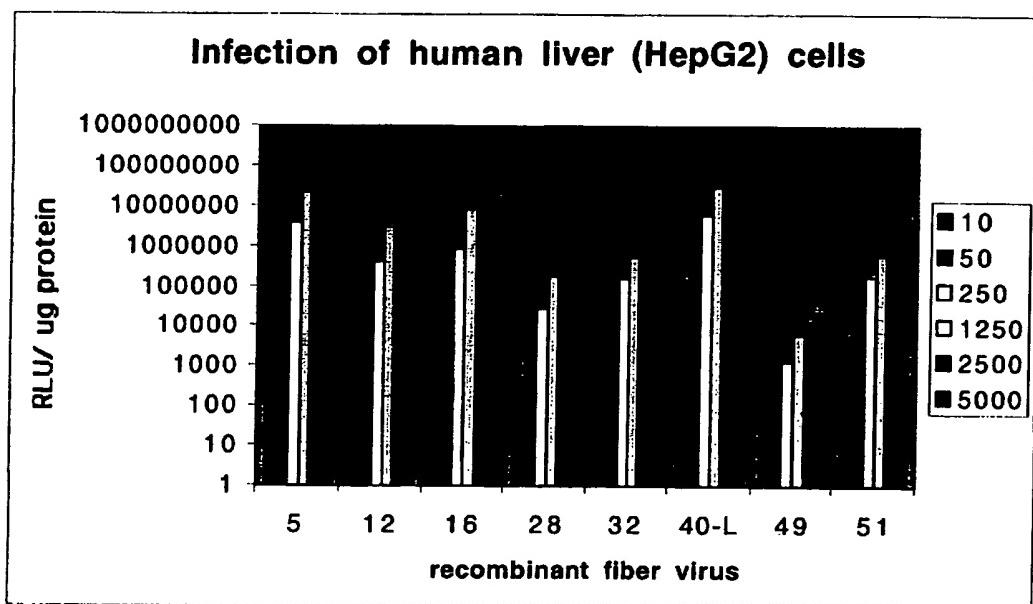


Figure 13





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Application Number

which under Rule 45 of the European Patent Convention EP 99 20 2234 shall be considered, for the purposes of subsequent proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT					
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.)		
X	WO 98 22609 A (ARMENTANO DONNA E ;GREGORY RICHARD J (US); GENZYME CORP (US); SMIT) 28 May 1998 (1998-05-28) * page 3, line 5 - line 12 * * page 3, line 22 - page 4, line 2 * * page 5, line 27 - page 9, line 2 * * page 9, line 26 - page 10, line 16 * * page 25; example 6 * * figures 4,5,7 * * sequences 2, 3 *	3,4, 7-14,17, 20-22 5,6	C12N15/34 C12N15/86 C12N15/10 A61K48/00 C07K14/705		
Y					
X	FALLAUX F ET AL: "New helper cells and matched early region 1-deleted adenovirus vectors prevent generation of replication-competent adenoviruses" HUMAN GENE THERAPY, vol. 9, no. 9, 1 September 1998 (1998-09-01), pages 1909-1917, XP002111070 ISSN: 1043-0342 * page 1909 * * abstract *	15,16 — — —/—	TECHNICAL FIELDS SEARCHED (Int.Cl.) C12N		
INCOMPLETE SEARCH					
The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.					
Claims searched completely :					
Claims searched incompletely :					
Claims not searched :					
Reason for the limitation of the search:					
see sheet C					
Place of search	Date of compilation of the search	Examiner			
THE HAGUE	8 June 2000	Sitch, W			
CATEGORY OF CITED DOCUMENTS					
X : particularly relevant if taken alone	T : theory or principle underlying the invention				
Y : particularly relevant if combined with another document of the same category	E : earlier patent document, but published on, or after the filing date				
A : technological background	D : document cited in the application				
O : non-written disclosure	L : document cited for other reasons				
P : intermediate document	& : member of the same patent family, corresponding document				

European Patent
OfficeINCOMPLETE SEARCH
SHEET CApplication Number
EP 99 20 2234

Although claims 1, 2 partially, insofar as such concern in vivo methods, are directed to a method of treatment of the human/animal body (Article 52(4) EPC), the search has been carried out and based on the alleged effects of the compound/composition.

Claim(s) not searched:
18, 19

Reason for the limitation of the search:

Present claims 18 and 19 relate to a compound (a cell receptor / binding site) defined by reference to a desirable characteristic or property, namely that such is for adenovirus type D and/or F, and is present on or is associated with CAR negative cells. No concrete structural data, or defining parameters, in relation to the cell receptor, are provided by the application. Example 7 on pages 43-45 of the application describes a protocol by which putative adherence molecules involved in adenovirus subgroup B, D and F binding and internalisation may be identified; no such identification / characterisation of the putative cell receptor or receptors is actually made however.

Claims 18 and 19 cover all compounds having the above-mentioned characteristics or properties, and yet the application provides no support within the meaning of Article 84 EPC and/or disclosure within the meaning of Article 83 EPC for any of such compounds which may fall under such a definition. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search of the claims is impossible. Consequently, no search has been carried out in respect of these claims.



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Application Number

EP 99 20 2234

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
X	PRING-AKERBLOM PATRICIA ET AL: "Characterization of adenovirus subgenus D fiber genes." VIROLOGY 1995, vol. 206, no. 1, 1995, pages 564-571, XP002139779 ISSN: 0042-6822 * page 568; figure 3 *	20-23	
X	MEI YA-FANG ET AL: "Highly heterogeneous fiber genes in the two closely related adenovirus genome types Ad35p and Ad34a." VIROLOGY 1995, vol. 206, no. 1, 1995, pages 686-689, XP002139780 ISSN: 0042-6822 * page 688; figure 2 *	20-23	
D,X	ARNBERG NIKLAS ET AL: "Fiber genes of adenoviruses with tropism for the eye and the genital tract." VIROLOGY 1997, vol. 227, no. 1, 1997, pages 239-244, XP002139781 ISSN: 0042-6822 * page 240; figure 1 *	20-23	
X	DATABASE EMBL SEQUENCE DATABASE 'Online! Hinxton, UK Accession no. 056784. TREMBL., 1 June 1998 (1998-06-01) PRING-AKERBLOM ET AL: "Human Adenovirus type 28 Fiber Protein" XP002139784 ---	20-23 -/-	



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Application Number

EP 99 20 2234

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.)
			TECHNICAL FIELDS SEARCHED (Int.Cl.)
X	DATABASE EMBL SEQUENCE DATABASE 'Online! Hinxton, UK Accession no. Q67733. TREMBL., 1 November 1996 (1996-11-01) BASLER ET AL: "Human Adenovirus Type 35 Fiber" XP002139785 ---	20-23	
X	DATABASE EMBL SEQUENCE DATABASE 'Online! Hinxton, UK Accession no. Q67712. TREMBL., 1 November 1996 (1996-11-01) SHIEH: "Human Adenovirus type 12 Fiber Protein" XP002139786 ---	20-23	
X	HUANG SHUANG ET AL: "A single amino acid in the adenovirus type 37 fiber confers binding to human conjunctival cells." JOURNAL OF VIROLOGY APRIL, 1999, vol. 73, no. 4, April 1999 (1999-04), pages 2798-2802, XP002139782 ISSN: 0022-538X * page 2798 * * abstract * * discussion * * page 2802 * ---	1,2 -/-	



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Application Number

EP 99 20 2234

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
Y	BASLER C F ET AL: "Sequence of the immunoregulatory early region 3 and flanking sequences of adenovirus type 35" GENE, NL, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 170, no. 2, 8 May 1996 (1996-05-08), pages 249-254, XP004042835 ISSN: 0378-1119 * page 249 * * abstract * * page 253, paragraph 3 - paragraph 4 * -----	5	
Y	WICKHAM T J ET AL: "Increased in vitro and in vivo gene transfer by adenovirus vectors containing chimeric fiber proteins" JOURNAL OF VIROLOGY, US, THE AMERICAN SOCIETY FOR MICROBIOLOGY, vol. 71, 1 November 1997 (1997-11-01), pages 8221-8229, XP002078898 ISSN: 0022-538X * page 8221 * * abstract * * page 8226, paragraph 7 - page 8227, paragraph 2 * -----	6	TECHNICAL FIELDS SEARCHED (Int.Cl.7)
Y	HIDAKA CHISA ET AL: "CAR-dependent and CAR-independent pathways of adenovirus vector-mediated gene transfer and expression in human fibroblasts." JOURNAL OF CLINICAL INVESTIGATION FEB., 1999, vol. 103, no. 4, February 1999 (1999-02), pages 579-587, XP002139783 ISSN: 0021-9738 * page 579 * * abstract * -----	6	

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ON EUROPEAN PATENT APPLICATION NO.

EP 99 20 2234

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The members are as contained in the European Patent Office EDP file on
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08-06-2000

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		AU 5455298 A	10-06-1998
		EP 0946742 A	06-10-1999

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82